GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 2, 2004, 19:31:09 ; Search time 16 Seconds
(without alignments)
781.761 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708	100.0	244	2	JC4708	gelatin-binding 28
2	297.5	42.0	674	2	S23297	collagen alpha 1(X
3	287.5	40.6	680	1	CGHU1D	collagen alpha 1(X
4	280.5	39.6	674	2	S13301	collagen alpha 1(X
5	280.5	39.6	680	2	S31216	collagen alpha 1(X
6	273.5	38.6	743	1	S23779	collagen alpha 1(V
7	270.5	38.2	744	2	S15435	collagen alpha 1(V
8	267.5	37.8	744	1	A34246	collagen alpha 1(V
9	263.5	37.2	744	1	S23298	collagen alpha 1(V
10	258.5	36.5	170	2	B57131	collagen alpha 2(V
11	258.5	36.5	635	2	A57131	collagen alpha 2(V
12	243.5	34.4	219	2	T14782	hypothetical prote
13	219	30.9	245	1	C1HUQC	complement subcomp
14	219	30.9	423	2	A55797	collagen precursor
15	208.5	29.4	246	2	S29328	complement subcomp
16	186	26.3	253	2	S49158	complement protein
17	184	26.0	253	2	I49560	complement C1q B c
18	182.5	25.8	253	1	C1HUQB	complement subcomp
19	178	25.1	215	2	B48150	hibernation-relate
20	176	24.9	196	2	A48150	hibernation-relate
21	174	24.6	215	2	C48150	hibernation-relate
22	156	22.0	245	2	S19018	complement subcomp
23	151.5	21.4	245	1	C1HUQA	complement subcomp
24	119.5	16.9	224	2	A60032	cerebellin-like gl
25	116.5	16.5	193	2	A37873	cerebellin precurs
26	113.5	16.0	1228	2	A57384	multimerin, endoth
27	86.5	12.2	213	2	B81360	probable protein d
28	82	11.6	280	1	G70126	phosphate ABC tran
29	77	10.9	687	2	E69733	PBSX prophage ORF
30	76	10.7	463	2	A38463	fibrinogen beta ch
31	76	10.7	1032	2	AI1697	alpha-mannosidase
32	75.5	10.7	527	2	T27572	hypothetical prote
33	74.5	10.5	1048	2	H64459	hypothetical prote
34	74	10.5	450	2	S57837	lymphoid-specific
35	74	10.5	992	2	T08772	hypothetical prote
36	74	10.5	1036	2	AG1326	alpha-mannosidase
37	73.5	10.4	1965	2	B98002	IgA-specific metal
38	73	10.3	366	2	B69949	phage-related prot
39	72.5	10.2	377	2	B55745	transcription fact
40	72	10.2	532	2	JC1392	monophenol monooxy
41	72	10.2	1797	2	F69195	cell surface glyco
42	71.5	10.1	183	2	A53516	ubiquitin-protein
43	71.5	10.1	183	2	JC4308	ubiquitin-protein
44	71.5	10.1	288	2	T33224	hypothetical prote
45	71.5	10.1	556	2	T03114	tegument protein -

ALIGNMENTS

RESULT 1
JC4708
gelatin-binding 28K protein precursor - human
N;Alternate names: adipose specific collagen-like factor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4708; JC4944
R;Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochem. Biophys. Res. Commun. 221, 286-289, 1996
A;Title: cDNA cloning and expression of a novel adipose specific collagen-like factor, ap
A;Reference number: JC4708; MUID:96224171; PMID:8619847
A;Accession: JC4708
A;Molecule type: mRNA
A;Residues: 1-244 <MAE>
A;Cross-references: UNIPROT:Q15848; DDBJ:D45371; NID:g871886; PIDN:BAA08227.1; PID:g87188
A;Experimental source: adipose tissue
R;Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.
J. Biochem. 120, 803-812, 1996
A;Title: Isolation and characterization of GBP28, a novel gelatin-binding protein purifie
A;Reference number: JC4944; MUID:97103474; PMID:8947845
A;Accession: JC4944
A;Molecule type: protein
A;Residues: 19-38;93-100;101-112;135-149;173-178 <NAK>
C;Comment: This protein is an endogenous factor that binds with a collagen-like domain. T
C;Genetics:
A;Gene: apM1
C;Keywords: adipose tissue; glycoprotein; hydroxyproline
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>
F;42-107/Region: collagen-like
F;114-241/Domain: complement C1q carboxyl-terminal homology <C1Q>
F;95/Modified site: 4-hydroxyproline (Pro) #status experimental
F;230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 708; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-63;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
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Db        115 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 174

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 234

Qy        121 TGFLLYHDTN 130
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Db        235 TGFLLYHDTN 244
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RESULT 2

S23297
collagen alpha 1(X) chain precursor - chicken
N;Alternate names: type X collagen
C;Species: Gallus gallus (chicken)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23297; A31896; S65594; S77711; I50218
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McQ
maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
A;Title: The molecular biology of collagens with short triple-helical domains.
A;Reference number: S22243
A;Accession: S23297
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-674 <NIN>
A;Cross-references: UNIPROT:P08125
R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A;Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
A;Reference number: A31896; MUID:89054019; PMID:2461368
A;Accession: A31896
A;Molecule type: mRNA
A;Residues: 1-75 <LUV>
R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.
J. Biol. Chem. 261, 5041-5050, 1986
A;Title: The developmentally regulated type X collagen gene contains a long open reading
A;Reference number: I50218; MUID:86168227; PMID:3082876
A;Accession: S65594
A;Molecule type: DNA
A;Residues: 'T',9,'D',11-12,'EDQMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVMADLVSSHT',48-89,'L',
629,'PQAVLSLISWRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <NIN1>
A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
A;Accession: S77711
A;Molecule type: protein
A;Residues: 104-112,'X',114-117;453-466 <NIN2>
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;
F;1-18/Domain: signal sequence #status predicted <SIG>
F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
F;453,456/Modified site: hydroxyproline (Pro) #status experimental
F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.0%; Score 297.5; DB 2; Length 674;
Best Local Similarity 47.6%; Pred. No. 6.8e-22;
Matches 59; Conservative 21; Mismatches 43; Indels 1; Gaps 1;

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Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:| |         :||:| || ||:| |||  || | | |||||||:||:    :| |:
Db        548 FTVILSKAYPGATVPIKFDKILYNRQQHYDPRTGIFTCRIPGLYYFSYHVHAKGTNVWVA 607

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:|    ::.:|||:||:  :|||||| :: |   ||||||:    | ||||:     |:|
Db        608 LYKNGSPVMYTYDEYQKGYLDQASGSAVIDLMENDQVWLQL-PNSESNGLYSSEYVHSSF 666

Qy        121 TGFL 124
              :|||
Db        667 SGFL 670
```

RESULT 3
CGHU1D
collagen alpha 1(X) chain precursor - human
N;Alternate names: procollagen alpha 1(X) chain
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
FEBS Lett. 311, 305-310, 1992
A;Title: Genomic organization and full-length cDNA sequence of human collagen X.
A;Reference number: S26396; MUID:93012005; PMID:1397333
A;Accession: S26396
A;Molecule type: DNA
A;Residues: 1-680 <REI>
A;Cross-references: UNIPROT:Q03692; EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; C
R;Apte, S.S.
submitted to the EMBL Data Library, March 1992
A;Reference number: S30085
A;Accession: S30086
A;Molecule type: DNA
A;Residues: 'TIPFYGWVCWVCLL',52-680 <APT>
A;Cross-references: EMBL:X65120; NID:g23129
A;Note: the initial difference is probably due to translation of an intronic sequence
R;Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
A;Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene to
A;Reference number: S15826; MUID:91243838; PMID:2037056
A;Accession: S15826
A;Molecule type: DNA
A;Residues: 561-647,'G',649-666 <AP2>
A;Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R;Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.
Biochem. J. 280, 617-623, 1991
A;Title: The human collagen X gene. Complete primary translated sequence and chromosomal
A;Reference number: S18249; MUID:92109659; PMID:1764025
A;Accession: S18249
A;Molecule type: DNA
A;Residues: 1-26,'T',28-680 <THO>
A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ala
R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A;Title: In situ hybridization studies on the expression of type X collagen in fetal huma
A;Reference number: A43901; MUID:92077285; PMID:1743401
A;Accession: A43901
A;Molecule type: mRNA
A;Residues: 547-656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
R;Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.E.
Am. J. Hum. Genet. 54, 169-178, 1994
A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain o
pe Schmid.
A;Reference number: I51870; MUID:94136476; PMID:8304336
A;Accession: I51870
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
A;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: GDB:COL10A1
A;Cross-references: GDB:128635; OMIM:120110
A;Map position: 6q21-6q22
A;Introns: 52/1
A;Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
C;Complex: type X collagen may be a homotrimer
C;Function:
A;Description: structural component of extracellular fibrous polymer specifically and tra
be important for skeletogenesis
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine; h
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
F;57-519/Region: interrupted helical
F;520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
F;617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.6%; Score 287.5; DB 1; Length 680;
Best Local Similarity 46.4%; Pred. No. 6.9e-21;
Matches 58; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

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Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:| |          || | || ||:| |||   || | | |||:|||:||: |     | |
Db        554 FTVILSKAYPAIGTPIPFDKILYNRQQHYDPRTGIFTCQIPGIYYFSYHVHVKGTHVWVG 613

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:|    :::|||:| :  :|||||| :: |    ||||||:    | ||||:     |:|
Db        614 LYKNGTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQL-PNAESNGLYSSEYVHSSF 672

Qy        121 TGFLL 125
              :|||:
Db        673 SGFLV 677


RESULT 4
S13301
collagen alpha 1(X) chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S13301
R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
Biochem. J. 273, 141-148, 1991
A;Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. Ev
A;Reference number: S13301; MUID:91113131; PMID:1703407
A;Accession: S13301
A;Molecule type: mRNA
A;Residues: 1-674 <THO>
A;Cross-references: UNIPROT:P23206; EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
C;Genetics:
A;Gene: COL10A1
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>

  Query Match           39.6%;  Score 280.5;  DB 2;  Length 674;
  Best Local Similarity  46.4%;  Pred. No. 3.5e-20;
  Matches   58;  Conservative   18;  Mismatches   48;  Indels    1;  Gaps    1;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:| |          || | || ||:| |||   || | | |||:|||:||| |     |
Db        548 FTVILSKAYPAIGTPIPFDKILYNKQQHYDPRTGIFTCKIPGIYYFSYHIHVKGTHAWVG 607

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:|    :::|||:| :  :|||||| :: |    |||||:    |  ||||:     |:|
Db        608 LYKNGTPVMYTYDEYIKGYLDQASGSAVIDLTENDQVWLQLPNAGS-NGLYSPEYVHSSF 666

Qy        121 TGFLL 125
              :|||:
Db        667 SGFLV 671


RESULT 5
S31216
collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; C
Eur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse
A;Reference number: S31216; MUID:93238750; PMID:8477738
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: UNIPROT:Q05306; EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cro
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S28807
A;Molecule type: DNA
A;Residues: 1-285,'A',287-680 <ELI>
A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Cron
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene.
A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L'
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse ty
A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'F
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Accession: S26397
A;Molecule type: protein
A;Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
C;Genetics:
A;Gene: Col10a-1
A;Map position: 10
A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

  Query Match           39.6%;  Score 280.5;  DB 2;  Length 680;
  Best Local Similarity  44.8%;  Pred. No. 3.5e-20;
  Matches   56;  Conservative   20;  Mismatches   48;  Indels    1;  Gaps    1;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:| |          || | :| ||:| |||   :| | | |||:|||:||: |     | |
Db        554 FTVILSKAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHVHVKGTHVWVG 613

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:|     ::|||:| :  :|||||| :: |    ||||||:    | ||||:     |:|
Db        614 LYKNGTPTMYTYDEYSKGYLDQASGSAIMELTENDQVWLQL-PNAESNGLYSSEYVHSSF 672

Qy        121 TGFLL 125
              :|||:
Db        673 SGFLV 677


RESULT 6
S23779
collagen alpha 1(VIII) chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S23779
R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.
Eur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypeptic
A;Reference number: S23779; MUID:92362626; PMID:1499564
A;Accession: S23779
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-743 <MUR>
A;Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g13599
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 38.6%; Score 273.5; DB 1; Length 743;
Best Local Similarity 45.1%; Pred. No. 2e-19;
Matches 55; Conservative 27; Mismatches 35; Indels 5; Gaps 2;

```
Qy          9 VTIP----NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKK 64
              :|:|      |::| |: || : :|:  || | | :||:||||||:     :| |:||| 
Db        621 LTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKN 680

Qy         65 DKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFL 124
              :: |::|||:|::  :|||||| :| |  ||||:||   | :  ||||     |:|:|:| 
Db        681 NEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQNPFE-QAAGLYAGQYVHSSFSGYL 739

Qy        125 LY 126
              || 
Db        740 LY 741
```

RESULT 7
S15435
collagen alpha 1(VIII) chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15435
R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y.
Eur. J. Biochem. 197, 615-622, 1991
A;Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
A;Reference number: S15435; MUID:91231001; PMID:2029894
A;Accession: S15435
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-744 <MUR>
A;Cross-references: UNIPROT:P27658; EMBL:X57527; NID:g30081; PIDN:CAA40748.1; PID:g30082
C;Genetics:
A;Gene: GDB:COL8A1
A;Cross-references: GDB:128104; OMIM:120251
A;Map position: 3q11.1-3q13.2
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 38.2%; Score 270.5; DB 2; Length 744;
Best Local Similarity 45.5%; Pred. No. 3.9e-19;
Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;

```
Qy         15 PIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAMLFTYDQ 74
              |:|| |: || : :|:  || | | :||:|||||||:     :| |:||| :: :::|||:
Db        632 PVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDE 691

Qy         75 YQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 126
              |::  :|||||| :| |  ||:|:||  | :  ||||     |:|:|:|||
Db        692 YKKGFLDQASGSAVLLLRPGDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY 742
```

RESULT 8
A34246
collagen alpha 1(VIII) chain precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34246
R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.
J. Biol. Chem. 264, 16022-16029, 1989
A;Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type
omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2476437
A;Accession: A34246
A;Molecule type: mRNA
A;Residues: 1-744 <YAM>
A;Cross-references: UNIPROT:P14282; GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 37.8%; Score 267.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 7.9e-19;
Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;

```
Qy         15 PIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAMLFTYDQ 74
              ||:| :: || : :|:  || | | :||:|||||||:     :| |:||| :: :::|||:
Db        632 PIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDE 691

Qy         75 YQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 126
              |::  :|||||| :| |  ||:|:||  | :  ||||     |:|:|:|||
Db        692 YKKGFLDQASGSAVLLLRPGDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY 742
```

RESULT 9
S23298
collagen alpha 1(VIII) chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S23298
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McCa
maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pres
A;Title: The molecular biology of collagens with short triple-helical domains.
A;Reference number: S22243
A;Accession: S23298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <NIN>
A;Cross-references: UNIPROT:Q7LZR2.
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 37.2%; Score 263.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 2e-18;
Matches 51; Conservative 27; Mismatches 33; Indels 1; Gaps 1;

```
Qy         15 PIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAMLFTYDQ 74
              ||:| :: || : :|:  || | | :||:|||||||:     :| |:||| :: :::|||:
Db        632 PIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDE 691

Qy         75 YQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 126
              |::  :|||||| :| |  ||:|:||  | :  ||||     |:|:|:|||
Db        692 YKKGFLDQASGSAVLLLRPGDRVFLQNPSE-QAAGLYAGQYVHSSFSGYLLY 742
```

RESULT 10
B57131
collagen alpha 2(VIII) chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: B57131
R;Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen famil
A;Reference number: A57131; MUID:91210292; PMID:2019595
A;Accession: B57131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <MUR>
A;Cross-references: UNIPROT:P25318; GB:M60833

C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;43-169/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 36.5%; Score 258.5; DB 2; Length 170;
Best Local Similarity 40.8%; Pred. No. 1.1e-18;
Matches 51; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:  | :      ||:|| :  || : |: :|| | | : |:||||||: |   :| |:
Db         44 FTAVLTSPFPASGMPVRFDRTLYNGHSGYNPATGIFSCPVGGVYYFAYHVHVKGTNVWVA 103

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:| :    :|||:|::  :|||||  :| |   ||||:|:  : : ||||:     |:|
Db        104 LYKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQMPSD-QANGLYSTEYIHSSF 162

Qy        121 TGFLL 125
              :||||
Db        163 SGFLL 167
```

RESULT 11
A57131
collagen alpha 2(VIII) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57131
R;Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen fami
A;Reference number: A57131; MUID:91210292; PMID:2019595
A;Accession: A57131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-635 <MUR>
A;Cross-references: UNIPROT:P25067; GB:M60832; NID:g177178; PIDN:AAA62822.1; PID:g177179
C;Genetics:
A;Gene: GDB:COL8A2
A;Cross-references: GDB:127812; OMIM:120252
A;Map position: 1p34.3-1p32.3
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F;1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>
F;12-468/Region: interrupted helical
F;469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>
F;508-634/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 36.5%; Score 258.5; DB 2; Length 635;
Best Local Similarity 40.0%; Pred. No. 5.2e-18;
Matches 50; Conservative 29; Mismatches 45; Indels 1; Gaps 1;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              |:  | :      ||::| :  ||  : |: :|| | | : |:||||||: |   :| |:
Db        509 FTAVLTSPLPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHVHVKGTNVWVA 568

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              |:| :    :|||:|::  :|||||  :| |   ||||:|:  : : ||||:     |:|
Db        569 LYKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQIPSD-QANGLYSTEYIHSSF 627

Qy        121 TGFLL 125
              :||||
Db        628 SGFLL 632
```

RESULT 12
T14782
hypothetical protein DKFZp586B0621.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14782
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18184
A;Accession: T14782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <OTT>
A;Cross-references: UNIPROT:Q9BXJ0; EMBL:AL110261
A;Experimental source: adult uterus; clone DKFZp586B0621
C;Genetics:
A;Note: DKFZp586B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;
Best Local Similarity 42.1%; Pred. No. 4.7e-17;
Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

```
Qy          6 ETYVTIP-NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKK 64
              |: |  | : |: | :: |:| |||  |||| | :||:|||| | |||   ::  | |
Db         88 ESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKN 147

Qy         65 DKAMLFTYDQYQENNVDQA--SGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTG 122
              :: : :: |:      |  ||  :: ||  ||||:|| | |:  |:||    ||||:|
Db        148 GES-IASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGDYIGIYASIKTDSTFSG 205

Qy        123 FLLYHD 128
              ||:| | .
Db        206 FLVYSD 211
```

RESULT 13
C1HUQC
complement subcomponent C1q chain C precursor - human
N;Alternate names: complement subcomponent C1q gamma chain
C;Species: Homo sapiens (man)
C;Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: S14351; A03207
R;Sellar, G.C.; Blake, D.J.; Reid, K.B.M.
Biochem. J. 274, 481-490, 1991
A;Title: Characterization and organization of the genes encoding the A-, B- and C-chains
A;Reference number: S14350; MUID:91174759; PMID:1706597
A;Accession: S14351
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-245 <SEL>
A;Cross-references: UNIPROT:P02747
R;Reid, K.B.M.
Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like regions present in subc
A;Reference number: A90304; MUID:80020137; PMID:486087
A;Accession: A03207
A;Molecule type: protein
A;Residues: 29-56,'P',58-65,'K',67-71,'P',73-83,'K',85-86,'D',88-89,'N',91-122 <REI>
C;Comment: The first component of complement is a calcium-dependent complex of the three
ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.
C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfide-
dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after reduc
C;Genetics:
A;Gene: GDB:C1QG
A;Cross-references: GDB:128132; OMIM:120575
A;Map position: 1p36.3-1p34.1
A;Introns: 60/3
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal homo
C;Keywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyproline;
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-245/Product: complement subcomponent C1q chain B #status predicted <MAT>
F;31-114/Domain: collagenous, triple helix <COL>
F;121-244/Domain: complement C1q carboxyl-terminal homology <C1Q>
F;32/Disulfide bonds: interchain #status experimental
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experin
F;57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
F;75/Binding site: carbohydrate (Lys) (covalent) #status experimental

Query Match 30.9%; Score 219; DB 1; Length 245;
Best Local Similarity 40.8%; Pred. No. 1.6e-14;
Matches 53; Conservative 22; Mismatches 47; Indels 8; Gaps 5;

```
Qy          1 FSVGLETY-VTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKV 59
              |:|  :|:    ||  |||  :  | |  || ||||| | :|||||| || : :  :: |
```

```
Db        122 FTVTRQTHQPPAPNSLIRFNAVLTNPQGDYDTSTGKFTCKVPGLYYFVYHAS-HTANLCV 180

Qy         60 SLFKKD-KAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDS 118
              |::   | : |     : | |:  || ||| |:||::||| |    :  |:     :||
Db        181 LLYRSGVKVVTFCGHTSKTNQVN--SGGVLLRLQVGEEVWLAVNDYYDMVGI---QGSDS 235

Qy        119 TFTGFLLYHD 128
               |:||||: |
Db        236 VFSGFLLFPD 245


RESULT 14
A55797
collagen precursor, saccule-specific - bluegill
C;Species: Lepomis macrochirus (bluegill)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 15-Sep-2003
C;Accession: A55797
R;Davis, J.G.; Oberholtzer, J.C.; Burns, F.R.; Greene, M.I.
Science 267, 1031-1034, 1995
A;Title: Molecular cloning and characterization of an inner ear-specific structural prot
A;Reference number: A55797; MUID:95167486; PMID:7863331
A;Accession: A55797
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <DAV>
A;Cross-references: GB:U17431; NID:g687605; PIDN:AAA69978.1; PID:g687606
F;58-271/Domain: collagenous, triple helix #status predicted <COL>
F;281-410/Domain: complement C1q carboxyl-terminal homology <C1Q>

  Query Match             30.9%;  Score 219;  DB 2;  Length 423;
  Best Local Similarity   43.1%;  Pred. No. 3e-14;
  Matches   44;  Conservative   17;  Mismatches   39;  Indels    2;  Gaps    1;

Qy          1 FSVGL--ETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVK 58
              |||||         |::|::| |:||| : |:| :  ||:   ||:| |:|||||  : |:
Db        282 FSVGLFPSRSFPPPSLPVKFDKVFYNGEGHWDPTLNKFNVTYPGVYLFSYHITVRNRPVR 341

Qy         59 VSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQ 100
              :|        | | |     ::|||    ||||  ||||||:
Db        342 AALVVNGVRKLRTRDSLYGQDIDQASNLALLHLTDGDQVWLE 383


RESULT 15
S29328
complement subcomponent C1q chain C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29328
R;Petry, F.; Reid, K.B.M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
A;Title: Isolation, sequence analysis and characterization of cDNA clones coding for the
ecerebellin.
A;Reference number: S29328; MUID:93011118; PMID:1396691
A;Accession: S29328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <PET>
A;Cross-references: UNIPROT:Q02105; EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom
F;122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

  Query Match             29.4%;  Score 208.5;  DB 2;  Length 246;
  Best Local Similarity   38.8%;  Pred. No. 1.8e-13;
  Matches   45;  Conservative   23;  Mismatches   43;  Indels    5;  Gaps    3;

Qy         13 NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDKAMLFTY 72
              |  :||  :  | | ||: ||||| | :|||||| |: | :  :: | |   : | : ::
Db        136 NALVRFNSVVTNPQGHYNPSTGKFTCEVPGLYYFVYY-TSHTANLCVHL-NLNLARVASF 193

Qy         73 DQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 128
              :  |:   :||  || |: ||:||| |    : ||:     ::| |:||||: |
Db        194 CDHMFNSKQVSSGGALLRLQRGDEVWLSV---NDYNGMVGIEGSNSVFSGFLLFPD 246
```

Search completed: December 2, 2004, 19:35:07
Job time : 18 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 2, 2004, 19:26:59 ; Search time 68 Seconds
(without alignments)
685.806 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708	100.0	130	2	AAY01485	Aay01485 ApM1 prot
2	708	100.0	130	7	ADE93609	Ade93609 Human adi
3	708	100.0	137	7	ADE93608	Ade93608 Human adi
4	708	100.0	144	7	ADE93607	Ade93607 Human adi
5	708	100.0	145	7	ADE93613	Ade93613 Human adi
6	708	100.0	157	7	ADE93606	Ade93606 Human adi
7	708	100.0	163	7	ADE93612	Ade93612 Human adi
8	708	100.0	163	7	ADE93655	Ade93655 Human adi
9	708	100.0	187	7	ADE93615	Ade93615 Human adi
10	708	100.0	193	7	ADE93614	Ade93614 Human adi
11	708	100.0	203	7	ADE93605	Ade93605 Human adi
12	708	100.0	226	7	ADE93604	Ade93604 Human adi
13	708	100.0	231	2	AAY21808	Aay21808 Adipose m
14	708	100.0	231	4	AAB60347	Aab60347 Recombina
15	708	100.0	233	7	ADD93530	Add93530 Novel NOV
16	708	100.0	244	2	AAY21807	Aay21807 Adipose m
17	708	100.0	244	3	AAY71053	Aay71053 Human APM
18	708	100.0	244	3	AAY71035	Aay71035 Human APM
19	708	100.0	244	3	AAB30233	Aab30233 Human adi
20	708	100.0	244	4	AAB65828	Aab65828 Human adi
21	708	100.0	244	4	AAE05529	Aae05529 Human OBG
22	708	100.0	244	4	AAB49598	Aab49598 Human ACR
23	708	100.0	244	4	AAB50373	Aab50373 Human adi
24	708	100.0	244	4	AAB49592	Aab49592 Human ACR
25	708	100.0	244	5	ABB08223	Abb08223 Human apm
26	708	100.0	244	5	AAG80254	Aag80254 Human APM
27	708	100.0	244	6	ABP70915	Abp70915 APM1 prot
28	708	100.0	244	6	ABR42035	Abr42035 Human APM
29	708	100.0	244	6	ABU98378	Abu98378 Human adi
30	708	100.0	244	6	ABP70905	Abp70905 APM1 prot
31	708	100.0	244	6	AAO16570	Aao16570 APM1 secr
32	708	100.0	244	6	ABR39800	Abr39800 APM1 poly
33	708	100.0	244	6	ABR40088	Abr40088 APM1 prot
34	708	100.0	244	6	ABR40249	Abr40249 Human APM
35	708	100.0	244	6	AAO30071	Aao30071 Human OBG
36	708	100.0	244	6	AAE37142	Aae37142 Human APM
37	708	100.0	244	6	ABR40221	Abr40221 Human gen
38	708	100.0	244	6	ABR39850	Abr39850 APM1 poly
39	708	100.0	244	6	ABR44306	Abr44306 APM1 poly
40	708	100.0	244	6	ABP70910	Abp70910 APM1 prot
41	708	100.0	244	6	ABP97854	Abp97854 Amino aci
42	708	100.0	244	6	ABR40011	Abr40011 Human APM
43	708	100.0	244	6	ABR43906	Abr43906 APM1 poly
44	708	100.0	244	6	ABU08790	Abu08790 Adiponect
45	708	100.0	244	6	ABP98485	Abp98485 Amino aci

ALIGNMENTS

RESULT 1
AAY01485
ID AAY01485 standard; peptide; 130 AA.
XX
AC AAY01485;
XX
DT 21-MAY-1999 (first entry)
XX
DE ApM1 protein fragment (residues 115-244).
XX
KW Dietary lipid; liver; peripheral tissue; medicament; C1q complement;
KW partitioning; lipolysis stimulated receptor; LSR; hypertension; gC1q.R;
KW obesity; atherosclerosis; insulin resistance; obesity-related disease;
KW micoangiopathy; Type II diabetes; ocular lesion; renal lesion; cachexia;
KW neoplastic; eating disorder; ApM1.
XX
OS Homo sapiens.
XX
PN WO9907736-A2.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-IB001256.
XX
PR 06-AUG-1997; 97FR-00010088.
PR 22-APR-1998; 98FR-00005032.
XX
PA (GEST) GENSET.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Bihain B, Bougueleret L, Yen-Potin F;
XX
DR WPI; 1999-167364/14.
XX
PT Use of lipolysis stimulated receptor - for developing agents for
PT modulating partitioning of dietary lipids between the liver and
PT peripheral tissues, e.g. for treating obesity.
XX
PS Claim 6; Page 70; 77pp; English.
XX
CC The invention relates to agents which influence the partitioning of
CC dietary lipids between the liver and peripheral tissues for use as
CC medicaments. Sequences shown in AAY01481-488 that relate to C1q
CC complement family and two consensus sequences (AAY01499-500) are
CC potentially useful as such agents. Compounds that influences the
CC partitioning of dietary lipids between the liver and peripheral tissues
CC can be used in medicament for treating a condition in which the
CC partitioning of dietary lipids to the liver is abnormal. A polypeptide

CC having binding specificity for a gamma subunit of the lipolysis
CC stimulated receptor (LSR) or a gC1q.R or gC1q.R homologue can be used for
CC treatment of obesity, where the polypeptide is not a subunit of the LSR.
CC The agents which increase partitioning of dietary lipids to the liver can
CC be used for treating obesity-related atherosclerosis, obesity-related
CC insulin resistance, obesity-related hypertension, micoangiopathic lesions
CC resulting from obesity-related Type II diabetes, ocular lesions caused by
CC microangiopathy in obese individuals with Type II diabetes, and renal
CC lesions caused by microangiopathy in obese individuals with Type II
CC diabetes. Agents which decrease the partitioning of dietary lipids to the
CC liver can be used for treating cachexia in subjects with neoplastic or
CC para-neoplastic syndrome or eating disorders. The present sequence
CC represents a claimed peptide fragment of ApM1
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        121 TGFLLYHDTN 130
```

RESULT 2
ADE93609
ID ADE93609 standard; protein; 130 AA.
XX
AC ADE93609;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(115-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 14; SEQ ID NO 7; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        121 TGFLLYHDTN 130
```

RESULT 3
ADE93608
ID ADE93608 standard; protein; 137 AA.
XX
AC ADE93608;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(108-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.

XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 14; SEQ ID NO 6; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 137 AA;

Query Match 100.0%; Score 708; DB 7; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 67

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 127

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        128 TGFLLYHDTN 137
```

RESULT 4
ADE93607
ID ADE93607 standard; protein; 144 AA.
XX
AC ADE93607;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(101-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 5; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 708; DB 7; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.9e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 74

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 134

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        135 TGFLLYHDTN 144
```

RESULT 5
ADE93613
ID ADE93613 standard; protein; 145 AA.
XX
AC ADE93613;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(100-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 11; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 708; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.9e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 75

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 135

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        136 TGFLLYHDTN 145
```

RESULT 6
ADE93606
ID ADE93606 standard; protein; 157 AA.
XX
AC ADE93606;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(88-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 4; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,

CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 157 AA;

Query Match 100.0%; Score 708; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 87

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 147

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        148 TGFLLYHDTN 157
```

RESULT 7
ADE93612
ID ADE93612 standard; protein; 163 AA.
XX
AC ADE93612;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(82-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR N-PSDB; ADE93618.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 10; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 163 AA;

Query Match 100.0%; Score 708; DB 7; Length 163;
Best Local Similarity 100.0%; Pred. No. 4.6e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 93

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 153

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        154 TGFLLYHDTN 163
```

RESULT 8
ADE93655
ID ADE93655 standard; protein; 163 AA.
XX
AC ADE93655;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin Y111N-apM1(82-244) mutant protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; mutant;
KW mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX

PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR N-PSDB; ADE93667.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 38; SEQ ID NO 53; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1(82-244) mutant
CC protein of the invention.
XX
SQ Sequence 163 AA;

Query Match 100.0%; Score 708; DB 7; Length 163;
Best Local Similarity 100.0%; Pred. No. 4.6e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 93

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 153

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        154 TGFLLYHDTN 163
```

RESULT 9
ADE93615
ID ADE93615 standard; protein; 187 AA.
XX
AC ADE93615;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(58-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR N-PSDB; ADE93617.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 13; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 187 AA;

Query Match 100.0%; Score 708; DB 7; Length 187;
Best Local Similarity 100.0%; Pred. No. 5.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 117

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 177

Qy        121 TGFLLYHDTN 130
              ||||||||||
```

```
Db        178 TGFLLYHDTN 187

RESULT 10
ADE93614
ID   ADE93614 standard; protein; 193 AA.
XX
AC   ADE93614;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human adiponectin apM1(52-244) protein.
XX
KW   adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW   antirheumatic; antibacterial; antilipaemic; dermatological;
KW   immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW   atherosclerosis; cardiovascular disease; dyslipidaemia;
KW   rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW   sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW   myocardial infarction; inflammation; gene therapy; human; apM1;
KW   wild-type.
XX
OS   Homo sapiens.
XX
PN   WO2003055916-A2.
XX
PD   10-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-DK000897.
XX
PR   21-DEC-2001; 2001DK-00001952.
PR   21-DEC-2001; 2001US-0343482P.
PR   25-APR-2002; 2002DK-00000627.
PR   25-APR-2002; 2002US-0375492P.
PR   03-JUL-2002; 2002DK-00001036.
PR   03-JUL-2002; 2002US-0394117P.
PR   20-SEP-2002; 2002DK-00001385.
PR   20-SEP-2002; 2002US-0412169P.
XX
PA   (MAXY-) MAXYGEN APS.
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Rasmussen PB,  Andersen KV,  Pedersen AH,  Schambye HT,  Halkier T;
PI   Bogsnes A;
XX
DR   WPI; 2003-598262/56.
DR   N-PSDB; ADE93616.
XX
PT   New conjugate comprising an adiponectin polypeptide and a first non-
PT   polypeptide moiety, useful for preparing a composition for treating a
PT   mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS   Claim 44; SEQ ID NO 12; 184pp; English.
XX
CC   The invention relates to a novel conjugate comprising an adiponectin
CC   polypeptide and a first non-polypeptide moiety covalently attached to the
CC   adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC   acid residue having an attachment group for the first non-polypeptide
CC   moiety which has been introduced in a position where the parent
CC   adiponectin is occupied by a surface exposed amino acid residue. The
CC   conjugate of the invention demonstrates antiarteriosclerotic,
CC   antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC   dermatological, immunosuppressive, immunomodulator and anorectic
CC   activities and may be useful for treating diabetes, obesity,
CC   atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC   arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC   syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC   infarction and destructive processes related to activation of the
CC   inflammatory system, as well as during gene therapy procedures. The
CC   current sequence is that of the human adiponectin apM1 protein of the
CC   invention.
XX
SQ   Sequence 193 AA;

  Query Match           100.0%;  Score 708;  DB 7;  Length 193;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-78;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 123

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 183

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        184 TGFLLYHDTN 193


RESULT 11
ADE93605
ID   ADE93605 standard; protein; 203 AA.
XX
AC   ADE93605;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human adiponectin apM1(42-244) protein.
XX
KW   adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW   antirheumatic; antibacterial; antilipaemic; dermatological;
KW   immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW   atherosclerosis; cardiovascular disease; dyslipidaemia;
KW   rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW   sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW   myocardial infarction; inflammation; gene therapy; human; apM1;
KW   wild-type.
XX
OS   Homo sapiens.
XX
PN   WO2003055916-A2.
XX
PD   10-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-DK000897.
XX
PR   21-DEC-2001; 2001DK-00001952.
PR   21-DEC-2001; 2001US-0343482P.
PR   25-APR-2002; 2002DK-00000627.
PR   25-APR-2002; 2002US-0375492P.
PR   03-JUL-2002; 2002DK-00001036.
PR   03-JUL-2002; 2002US-0394117P.
PR   20-SEP-2002; 2002DK-00001385.
PR   20-SEP-2002; 2002US-0412169P.
XX
PA   (MAXY-) MAXYGEN APS.
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Rasmussen PB,  Andersen KV,  Pedersen AH,  Schambye HT,  Halkier T;
PI   Bogsnes A;
XX
DR   WPI; 2003-598262/56.
XX
PT   New conjugate comprising an adiponectin polypeptide and a first non-
PT   polypeptide moiety, useful for preparing a composition for treating a
PT   mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS   Claim 44; SEQ ID NO 3; 184pp; English.
XX
CC   The invention relates to a novel conjugate comprising an adiponectin
CC   polypeptide and a first non-polypeptide moiety covalently attached to the
CC   adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC   acid residue having an attachment group for the first non-polypeptide
CC   moiety which has been introduced in a position where the parent
```

```
CC   adiponectin is occupied by a surface exposed amino acid residue. The
CC   conjugate of the invention demonstrates antiarteriosclerotic,
CC   antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC   dermatological, immunosuppressive, immunomodulator and anorectic
CC   activities and may be useful for treating diabetes, obesity,
CC   atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC   arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC   syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC   infarction and destructive processes related to activation of the
CC   inflammatory system, as well as during gene therapy procedures. The
CC   current sequence is that of the human adiponectin apM1 protein of the
CC   invention.
XX
SQ   Sequence 203 AA;

  Query Match             100.0%;  Score 708;  DB 7;  Length 203;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-78;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 133

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 193

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        194 TGFLLYHDTN 203


RESULT 12
ADE93604
ID   ADE93604 standard; protein; 226 AA.
XX
AC   ADE93604;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human adiponectin apM1(19-244) protein.
XX
KW   adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW   antirheumatic; antibacterial; antilipaemic; dermatological;
KW   immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW   atherosclerosis; cardiovascular disease; dyslipidaemia;
KW   rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW   sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW   myocardial infarction; inflammation; gene therapy; human; apM1;
KW   wild-type.
XX
OS   Homo sapiens.
XX
PN   WO2003055916-A2.
XX
PD   10-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-DK000897.
XX
PR   21-DEC-2001; 2001DK-00001952.
PR   21-DEC-2001; 2001US-0343482P.
PR   25-APR-2002; 2002DK-00000627.
PR   25-APR-2002; 2002US-0375492P.
PR   03-JUL-2002; 2002DK-00001036.
PR   03-JUL-2002; 2002US-0394117P.
PR   20-SEP-2002; 2002DK-00001385.
PR   20-SEP-2002; 2002US-0412169P.
XX
PA   (MAXY-) MAXYGEN APS.
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Rasmussen PB,  Andersen KV,  Pedersen AH,  Schambye HT,  Halkier T;
PI   Bogsnes A;
XX
DR   WPI; 2003-598262/56.
XX
PT   New conjugate comprising an adiponectin polypeptide and a first non-
PT   polypeptide moiety, useful for preparing a composition for treating a
PT   mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS   Claim 14; SEQ ID NO 2; 184pp; English.
XX
CC   The invention relates to a novel conjugate comprising an adiponectin
CC   polypeptide and a first non-polypeptide moiety covalently attached to the
CC   adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC   acid residue having an attachment group for the first non-polypeptide
CC   moiety which has been introduced in a position where the parent
CC   adiponectin is occupied by a surface exposed amino acid residue. The
CC   conjugate of the invention demonstrates antiarteriosclerotic,
CC   antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC   dermatological, immunosuppressive, immunomodulator and anorectic
CC   activities and may be useful for treating diabetes, obesity,
CC   atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC   arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC   syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC   infarction and destructive processes related to activation of the
CC   inflammatory system, as well as during gene therapy procedures. The
CC   current sequence is that of the human adiponectin apM1 protein of the
CC   invention.
XX
SQ   Sequence 226 AA;

  Query Match             100.0%;  Score 708;  DB 7;  Length 226;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-78;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 156

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 216

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        217 TGFLLYHDTN 226


RESULT 13
AAY21808
ID   AAY21808 standard; protein; 231 AA.
XX
AC   AAY21808;
XX
DT   10-SEP-1999  (first entry)
XX
DE   Adipose most abundant gene transcription product 1 (apM1) fragment.
XX
KW   Smooth muscle proliferation; secretion factor; apM1; adipose;
KW   adipose most abundant gene transcription product 1; obesity;
KW   arteriosclerosis; restenosis; angina pectoris; myocardial infarction.
XX
OS   Unidentified.
XX
PN   WO9921577-A1.
XX
PD   06-MAY-1999.
XX
PF   27-OCT-1998;   98WO-JP004862.
XX
PR   29-OCT-1997;   97JP-00297569.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
PI   Matsuzawa Y,  Ohmoto Y;
```

XX
DR WPI; 1999-418412/35.
XX
PT Inhibition of smooth muscle proliferation using secretion factor apM1.
XX
PS Example; Page 59-60; 65pp; Japanese.
XX
CC Then invention relates to the inhibition of smooth muscle proliferation
CC using a composition containing secretion factor apM1 (adipose most
CC abundant gene transcriptio product 1), together with a suitable carrier.
CC apM1 is expressed specifically in adipose tissue and the composition is
CC used for the prevention and treatment of arteriosclerosis; restenosis
CC following vascular reconstruction; and treatment and diagnosis of
CC diseases related to obesity, and disorders associated with it such as
CC angina pectoris and myocardial infarction. The present sequence
CC represents a fragment of apM1 isolated from abdominal fat tissue of myoma
CC uteri
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 708; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
Db 102 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 161

Qy 61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
Db 162 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 221

Qy 121 TGFLLYHDTN 130
Db 222 TGFLLYHDTN 231

RESULT 14
AAB60347
ID AAB60347 standard; protein; 231 AA.
XX
AC AAB60347;
XX
DT 06-APR-2001 (first entry)
XX
DE Recombinant human apM1 protein (residues 15-244 + Met1), SEQ ID NO:3.
XX
KW Antigenic protein detection; sodium sulphate; ELISA;
KW enzyme-linked immunosorbent assay; human apM1; recombinant expression;
KW Escherichia coli; adipose most abundant gene transcript 1;
KW adipose-specific collagen-like factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2000304748-A.
XX
PD 02-NOV-2000.
XX
PF 21-APR-1999; 99JP-00114170.
XX
PR 21-APR-1999; 99JP-00114170.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
DR WPI; 2001-127687/14.
XX
PT Detection of an antigenic protein comprises use of enzyme linked
PT immunosorbant assay.
XX
PS Example 1; Page 7-8; 10pp; Japanese.
XX
CC The invention relates to a method for detecting an antigenic protein. The
CC method comprises boiling the sample containing the antigenic protein in
CC the presence of sodium sulphate, diluting it in buffer, and detecting the
CC enzyme by enzyme-linked immunosorbent assay (ELISA). In an
CC exemplification of the invention, residues 15-244 (plus an initial Met
CC residue) of human apM1 (adipose most abundant gene transcript 1;
CC AAB60347), an adipose-specific collagen-like factor, was recombinantly
CC expressed in Escherichia coli. Using the method of the invention, it was
CC found that apM1 was expressed mainly in the inclusion body fragment as an
CC approximately 30 kd protein. The present sequence represents the
CC recombinantly expressed human apM1
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
Db 102 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 161

Qy 61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
Db 162 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 221

Qy 121 TGFLLYHDTN 130
Db 222 TGFLLYHDTN 231

RESULT 15
ADD93530
ID ADD93530 standard; protein; 233 AA.
XX
AC ADD93530;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel NOV2e, homologous to human adiponectin.
XX
KW NOV2e; human; adiponectin; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003078572-A2.
XX
PD 25-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US006859.
XX
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 21-MAR-2002; 2002US-0366420P.
PR 05-MAR-2003; 2003US-00379747.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Gangolli EA;
PI Malyankar UM, Miller CE, Coi CE, Ort T, Patturajan M, Rastelli L;
PI Rieger DK, Shimkets RA, Zerhusen BD;
XX
DR WPI; 2003-779122/73.
DR N-PSDB; ADD93529.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; Page 108; 205pp; English.
XX
CC The present sequence is the protein sequence of a novel polypeptide,
CC designated NOV2e, that shows amino acid sequence homology to the human

CC adiponectin (adipose most abundant gene transcript 1, APM1). The
CC adiponectin gene is the most abundant gene transcript in adipose cells
CC that regulates lipid metabolism. An interaction between adiponectin and
CC calcium modulating ligand was identified, indicating a novel pathway by
CC which adiponectin may induce lipid breakdown in muscle cells and
CC adipocytes. The invention is based on the identification of proteins and
CC polypeptides, and the nucleic acids encoding them, that are
CC differentially modulated in a pathological state, disease or an abnormal
CC condition or state. These are targets for therapeutic agents and can be
CC used in screening methodologies to identify candidate therapeutic agents
CC which interact with the target and thereby exert a desired or favourable
CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
CC haematopoiesis, wound healing and angiogenesis. Methods for diagnosis,
CC treatment and prevention of disorders involving the novel human nucleic
CC acids and proteins are provided. The polypeptides are also used to raise
CC antibodies, useful in therapy and diagnosis.
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 708; DB 7; Length 233;
Best Local Similarity 100.0%; Pred. No. 7.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
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Db        164 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 223

Qy        121 TGFLLYHDTN 130
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Db        224 TGFLLYHDTN 233
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Search completed: December 2, 2004, 19:33:35
Job time : 71 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 2, 2004, 19:32:25 ; Search time 144 Seconds
(without alignments)
321.951 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708	100.0	130	13	US-10-072-159-11	Sequence 11, Appl
2	708	100.0	130	13	US-10-060-845-11	Sequence 11, Appl
3	708	100.0	130	14	US-10-325-717-7	Sequence 7, Appli
4	708	100.0	137	14	US-10-325-717-6	Sequence 6, Appli
5	708	100.0	144	14	US-10-325-717-5	Sequence 5, Appli
6	708	100.0	145	14	US-10-325-717-11	Sequence 11, Appl
7	708	100.0	157	14	US-10-325-717-4	Sequence 4, Appli
8	708	100.0	163	14	US-10-325-717-10	Sequence 10, Appl
9	708	100.0	163	14	US-10-325-717-53	Sequence 53, Appl
10	708	100.0	187	14	US-10-325-717-13	Sequence 13, Appl
11	708	100.0	193	14	US-10-325-717-12	Sequence 12, Appl
12	708	100.0	203	14	US-10-325-717-3	Sequence 3, Appli
13	708	100.0	226	14	US-10-325-717-2	Sequence 2, Appli
14	708	100.0	231	14	US-10-189-493-2	Sequence 2, Appli
15	708	100.0	233	15	US-10-379-747-14	Sequence 14, Appl
16	708	100.0	244	9	US-09-776-976-6	Sequence 6, Appli
17	708	100.0	244	9	US-09-758-055-6	Sequence 6, Appli
18	708	100.0	244	9	US-09-909-547-6	Sequence 6, Appli
19	708	100.0	244	9	US-09-911-176B-48	Sequence 48, Appl
20	708	100.0	244	14	US-10-180-762-51	Sequence 51, Appl
21	708	100.0	244	14	US-10-231-814-6	Sequence 6, Appli
22	708	100.0	244	14	US-10-234-000-4	Sequence 4, Appli
23	708	100.0	244	14	US-10-360-186-51	Sequence 51, Appl
24	708	100.0	244	14	US-10-321-164-3	Sequence 3, Appli
25	708	100.0	244	14	US-10-376-460-6	Sequence 6, Appli
26	708	100.0	244	14	US-10-189-493-1	Sequence 1, Appli
27	708	100.0	244	14	US-10-197-293-3	Sequence 3, Appli
28	708	100.0	244	14	US-10-325-717-1	Sequence 1, Appli
29	708	100.0	244	14	US-10-411-120-67	Sequence 67, Appl
30	708	100.0	244	15	US-10-379-747-6	Sequence 6, Appli
31	708	100.0	244	15	US-10-379-747-8	Sequence 8, Appli
32	708	100.0	244	15	US-10-379-747-10	Sequence 10, Appl
33	708	100.0	244	15	US-10-621-787-3	Sequence 3, Appli
34	708	100.0	244	15	US-10-285-833-6	Sequence 6, Appli
35	708	100.0	250	15	US-10-379-747-12	Sequence 12, Appl
36	703	99.3	145	14	US-10-325-717-27	Sequence 27, Appl
37	703	99.3	163	14	US-10-325-717-18	Sequence 18, Appl
38	703	99.3	163	14	US-10-325-717-55	Sequence 55, Appl
39	703	99.3	163	14	US-10-325-717-60	Sequence 60, Appl
40	703	99.3	187	14	US-10-325-717-33	Sequence 33, Appl
41	703	99.3	193	14	US-10-325-717-30	Sequence 30, Appl
42	703	99.3	203	14	US-10-325-717-21	Sequence 21, Appl
43	702	99.2	144	14	US-10-325-717-25	Sequence 25, Appl
44	702	99.2	145	14	US-10-325-717-26	Sequence 26, Appl
45	702	99.2	145	14	US-10-325-717-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-072-159-11
; Sequence 11, Application US/10072159
; Publication No. US20020151498A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET.036APC
; CURRENT APPLICATION NUMBER: US/10/072,159
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-072-159-11

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 6.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
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Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
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Db         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120

Qy        121 TGFLLYHDTN 130
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Db        121 TGFLLYHDTN 130


RESULT 2
US-10-060-845-11
; Sequence 11, Application US/10060845
; Publication No. US20020165154A1
; GENERAL INFORMATION:
;  APPLICANT: Bihain, Bernard
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Yen-Potin, Frances
;  TITLE OF INVENTION: Lipoprotein-regulating medicaments
;  FILE REFERENCE: GENSET.036APC
;  CURRENT APPLICATION NUMBER: US/10/060,845
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: U.S. 09/485,316
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: FR 97/10088
;  PRIOR FILING DATE: 1997-08-06
;  PRIOR APPLICATION NUMBER: FR 98/05032
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: PCT IB98/01256
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: Patent.pm
; SEQ ID NO 11
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: 1..130
;   OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-060-845-11

  Query Match           100.0%;  Score 708;  DB 13;  Length 130;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-70;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
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Db          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
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Qy        121 TGFLLYHDTN 130
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Db        121 TGFLLYHDTN 130


RESULT 3
US-10-325-717-7
; Sequence 7, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(115-244)
US-10-325-717-7

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  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
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Db         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120

Qy        121 TGFLLYHDTN 130
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Db        121 TGFLLYHDTN 130


RESULT 4
US-10-325-717-6
; Sequence 6, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
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;   FEATURE:
;   OTHER INFORMATION: apM1(108-244)
US-10-325-717-6

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Qy        121 TGFLLYHDTN 130
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RESULT 5
US-10-325-717-5
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; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(101-244)
US-10-325-717-5

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  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
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Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
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Db         75 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 134

Qy        121 TGFLLYHDTN 130
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Db        135 TGFLLYHDTN 144


RESULT 6
US-10-325-717-11
; Sequence 11, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
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; SEQ ID NO 11
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;   FEATURE:
;   OTHER INFORMATION: apM1(100-244)
US-10-325-717-11

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Db         76 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 135

Qy        121 TGFLLYHDTN 130
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Db        136 TGFLLYHDTN 145


RESULT 7
US-10-325-717-4
; Sequence 4, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
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;   FEATURE:
;   OTHER INFORMATION: apM1(88-244)
US-10-325-717-4
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  Query Match           100.0%;  Score 708;  DB 14;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-70;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 87

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 147

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        148 TGFLLYHDTN 157


RESULT 8
US-10-325-717-10
; Sequence 10, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 163
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(82-244)
US-10-325-717-10

  Query Match           100.0%;  Score 708;  DB 14;  Length 163;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-70;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 93

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 153

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        154 TGFLLYHDTN 163


RESULT 9
US-10-325-717-53
; Sequence 53, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;   LENGTH: 163
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct Y111N-apM1(82-244)
US-10-325-717-53

  Query Match           100.0%;  Score 708;  DB 14;  Length 163;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-70;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 93

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 153

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        154 TGFLLYHDTN 163


RESULT 10
US-10-325-717-13
; Sequence 13, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 187
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(58-244)
US-10-325-717-13

  Query Match           100.0%;  Score 708;  DB 14;  Length 187;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-70;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 117

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 177

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        178 TGFLLYHDTN 187


RESULT 11
US-10-325-717-12
; Sequence 12, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(52-244)
US-10-325-717-12

  Query Match           100.0%;  Score 708;  DB 14;  Length 193;
  Best Local Similarity  100.0%;  Pred. No. 1e-69;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 123

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 183

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        184 TGFLLYHDTN 193


RESULT 12
US-10-325-717-3
; Sequence 3, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 203
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(42-244)
US-10-325-717-3

  Query Match           100.0%;  Score 708;  DB 14;  Length 203;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-69;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 133

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 193

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        194 TGFLLYHDTN 203


RESULT 13
US-10-325-717-2
; Sequence 2, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: apM1(19-244)
US-10-325-717-2

  Query Match           100.0%;  Score 708;  DB 14;  Length 226;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-69;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 156

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 216

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        217 TGFLLYHDTN 226


RESULT 14
US-10-189-493-2
; Sequence 2, Application US/10189493
; Publication No. US20030166551A1
; GENERAL INFORMATION:
;  APPLICANT: Otsuka Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
;  TITLE OF INVENTION:  diagnostic method for arteriosclerosis and a kit
;  TITLE OF INVENTION:  therefor
;  FILE REFERENCE: P98-51
;  CURRENT APPLICATION NUMBER: US/10/189,493
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: US/09/530,423
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 231
;   TYPE: PRT
;   ORGANISM: Abdominal fat tissue from myoma uteri
US-10-189-493-2

  Query Match           100.0%;  Score 708;  DB 14;  Length 231;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-69;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 161

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 221

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        222 TGFLLYHDTN 231


RESULT 15
US-10-379-747-14
; Sequence 14, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E.;
;  APPLICANT:  Chant, John S.;
;  APPLICANT:  Chaudhuri, Amitabha ;
;  APPLICANT:  Edinger, Shlomit R.;
;  APPLICANT:  Gangolli, Esha A.;
;  APPLICANT:  Malyankar, Uriel M.;
;  APPLICANT:  Miller, Charles E.;
;  APPLICANT:  Ooi, Chean Eng;
;  APPLICANT:  Ort, Tatiana A.;
;  APPLICANT:  Patturajan, Meera ;
;  APPLICANT:  Rastelli, Luca ;
;  APPLICANT:  Rieger, Daniel K.;
;  APPLICANT:  Shimkets, Richard A.;
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-568B
;  CURRENT APPLICATION NUMBER: US/10/379,747
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/365,034
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: 60/366,420
;  PRIOR FILING DATE: 2002-03-21
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-747-14

  Query Match           100.0%;  Score 708;  DB 15;  Length 233;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-69;
  Matches  130;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 FSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVS 163

Qy         61 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 LFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTF 223

Qy        121 TGFLLYHDTN 130
              ||||||||||
Db        224 TGFLLYHDTN 233


Search completed: December  2, 2004, 19:38:04
Job time : 145 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:18:03 ; Search time 399 Seconds
(without alignments)
1710.338 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10072159/runat_02122004_142304_15552/app_query.fasta_1.327
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10072159_@CGN_1_1_708_@runat_02122004_142304_15552 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708	100.0	492	10	ADE93618	Ade93618 Human adi
2	708	100.0	537	10	ADE93667	Ade93667 Human adi
3	708	100.0	564	10	ADE93617	Ade93617 Human adi
4	708	100.0	582	10	ADE93616	Ade93616 Human adi
5	708	100.0	735	8	AAD56155	Aad56155 Human APM
6	708	100.0	735	10	ADC21966	Adc21966 Human ins
7	708	100.0	735	10	ADF16357	Adf16357 Human alb
8	708	100.0	735	10	ADF16359	Adf16359 Human alb
9	708	100.0	735	10	ADF16358	Adf16358 Human alb
10	708	100.0	735	10	ADE93611	Ade93611 Human adi
11	708	100.0	735	10	ADH21732	Adh21732 Human adi
12	708	100.0	735	10	ADH21734	Adh21734 Human HDA
13	708	100.0	735	10	ADH21733	Adh21733 Human HDA
14	708	100.0	735	12	ADF14853	Adf14853 Human art
15	708	100.0	742	10	ADD93529	Add93529 Novel nuc
16	708	100.0	754	10	ADD93525	Add93525 Novel nuc
17	708	100.0	778	10	ADD93527	Add93527 Novel nuc
18	708	100.0	783	10	ADD93521	Add93521 Novel nuc
19	708	100.0	1550	10	ADF94923	Adf94923 Human gen
20	708	100.0	4517	4	AAD10373	Aad10373 Human APM
21	708	100.0	4517	6	ABL67201	Abl67201 Thyroid c
22	708	100.0	4517	6	ABA96120	Aba96120 Human apm
23	708	100.0	4517	6	ABT10832	Abt10832 Human bre
24	708	100.0	4517	8	AAL60689	Aal60689 Human OBG
25	708	100.0	4517	12	ADF72537	Adf72537 Human OBG
26	708	100.0	4517	12	ADG14698	Adg14698 Human OBG
27	708	100.0	4517	12	ADQ18230	Adq18230 Human sof
28	708	100.0	4517	12	ADQ22777	Adq22777 Human sof
29	708	100.0	4545	3	AAD00553	Aad00553 Human APM
30	708	100.0	4545	6	AAI69247	Aai69247 Human APM
31	708	100.0	4545	10	ADD93523	Add93523 Novel nuc
32	708	100.0	20966	3	AAD00552	Aad00552 Human APM
33	708	100.0	20966	4	AAD10374	Aad10374 Human APM
34	708	100.0	20966	6	ABA96121	Aba96121 Human nuc
35	708	100.0	20966	6	AAI69243	Aai69243 Human APM
36	708	100.0	20966	8	AAL60690	Aal60690 Human OBG
37	708	100.0	20966	12	ADF72541	Adf72541 Human OBG
38	703	99.3	537	10	ADE93670	Ade93670 Human adi
39	703	99.3	537	10	ADE93665	Ade93665 Human adi
40	702	99.2	537	10	ADE93664	Ade93664 Human adi
41	702	99.2	537	10	ADE93666	Ade93666 Human adi
42	701	99.0	1313	2	AAT51049	Aat51049 Human adi
43	700	98.9	537	10	ADE93669	Ade93669 Human adi
44	699	98.7	411	10	ACC83228	Acc83228 N-termina
45	699	98.7	537	10	ADE93671	Ade93671 Human adi

ALIGNMENTS

RESULT 1
ADE93618
ID ADE93618 standard; cDNA; 492 BP.
XX
AC ADE93618;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(82-244) cDNA.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR P-PSDB; ADE93612.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 63; SEQ ID NO 16; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 cDNA of the
CC invention.
XX
SQ Sequence 492 BP; 130 A; 128 C; 119 G; 115 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.88e-86	Length:	492
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADE93618 (1-492)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 159

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 219

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 279

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 339

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 399

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 459

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        460 ACAGGCTTTCTTCTCTACCATGACACCAAC 489
```

RESULT 2
ADE93667
ID ADE93667 standard; cDNA; 537 BP.
XX
AC ADE93667;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin Y111N-apM1(82-244) mutant cDNA.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; mutant;
KW ss; gene.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR P-PSDB; ADE93655.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 63; SEQ ID NO 65; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The

CC current sequence is that of the human adiponectin apM1(82-244) mutant
CC cDNA of the invention.
XX
SQ Sequence 537 BP; 135 A; 139 C; 132 G; 131 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.9e-86	Length:	537
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADE93667 (1-537)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 204

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 264

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 324

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 384

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 444

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 504

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        505 ACAGGCTTTCTTCTCTACCATGACACCAAC 534
```

RESULT 3
ADE93617
ID ADE93617 standard; cDNA; 564 BP.
XX
AC ADE93617;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(58-244) cDNA.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR P-PSDB; ADE93615.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 63; SEQ ID NO 15; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 cDNA of the
CC invention.
XX
SQ Sequence 564 BP; 150 A; 140 C; 145 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.53e-86	Length:	564
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADE93617 (1-564)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 231

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 291

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 351

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 411

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 471

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        472 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 531

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              |||||||||||||||||||||||||||||
Db        532 ACAGGCTTTCTTCTCTACCATGACACCAAC 561

RESULT 4
ADE93616
ID   ADE93616 standard; cDNA; 582 BP.
XX
AC   ADE93616;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human adiponectin apM1(52-244) cDNA.
XX
KW   adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW   antirheumatic; antibacterial; antilipaemic; dermatological;
KW   immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW   atherosclerosis; cardiovascular disease; dyslipidaemia;
KW   rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW   sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW   myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
KW   wild-type.
XX
OS   Homo sapiens.
XX
PN   WO2003055916-A2.
XX
PD   10-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-DK000897.
XX
PR   21-DEC-2001; 2001DK-00001952.
PR   21-DEC-2001; 2001US-0343482P.
PR   25-APR-2002; 2002DK-00000627.
PR   25-APR-2002; 2002US-0375492P.
PR   03-JUL-2002; 2002DK-00001036.
PR   03-JUL-2002; 2002US-0394117P.
PR   20-SEP-2002; 2002DK-00001385.
PR   20-SEP-2002; 2002US-0412169P.
XX
PA   (MAXY-) MAXYGEN APS.
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Rasmussen PB,  Andersen KV,  Pedersen AH,  Schambye HT,  Halkier T;
PI   Bogsnes A;
XX
DR   WPI; 2003-598262/56.
DR   P-PSDB; ADE93614.
XX
PT   New conjugate comprising an adiponectin polypeptide and a first non-
PT   polypeptide moiety, useful for preparing a composition for treating a
PT   mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS   Claim 63; SEQ ID NO 14; 184pp; English.
XX
CC   The invention relates to a novel conjugate comprising an adiponectin
CC   polypeptide and a first non-polypeptide moiety covalently attached to the
CC   adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC   acid residue having an attachment group for the first non-polypeptide
CC   moiety which has been introduced in a position where the parent
CC   adiponectin is occupied by a surface exposed amino acid residue. The
CC   conjugate of the invention demonstrates antiarteriosclerotic,
CC   antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC   dermatological, immunosuppressive, immunomodulator and anorectic
CC   activities and may be useful for treating diabetes, obesity,
CC   atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC   arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC   syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC   infarction and destructive processes related to activation of the
CC   inflammatory system, as well as during gene therapy procedures. The
CC   current sequence is that of the human adiponectin apM1 cDNA of the
CC   invention.
XX
SQ   Sequence 582 BP; 152 A; 147 C; 152 G; 131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.96e-86        Length:          582
Score:                    708.00          Matches:         130
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       10              Gaps:            0

US-10-072-159-11 (1-130) x ADE93616 (1-582)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 249

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 309

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 369

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 429

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 489

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 549

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              |||||||||||||||||||||||||||||
Db        550 ACAGGCTTTCTTCTCTACCATGACACCAAC 579

RESULT 5
AAD56155
ID   AAD56155 standard; DNA; 735 BP.
XX
AC   AAD56155;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human APM1 DNA.
XX
KW   Human; Genset zinc-alpha-2-glycoprotein interacting protein; GZIP; ZAG;
KW   metabolic-related disease; obesity; impaired glucose tolerance; fat mass;
KW   body mass; lean muscle mass; insulin tolerance; atherosclerosis; stroke;
KW   heart disease; hypertension; type II diabetes; protein therapy; cardiant;
KW   glomerulonephritis; hypotensive; cerebroprotective; antiinflammatory;
KW   APM1; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .735
FT                   /*tag= a
FT                   /product= "Human APM1 protein"
XX
PN   WO2003033534-A2.
XX
PD   24-APR-2003.
XX
PF   03-OCT-2002; 2002WO-IB004635.
XX
PR   12-OCT-2001; 2001US-0329074P.
```

```
XX
PA   (GEST ) GENSET SA.
XX
PI   Scalia A,  Dialynas D,  Briggs K;
XX
DR   WPI; 2003-393503/37.
DR   P-PSDB; AAE37142.
XX
PT   New NGZIPA, NGZIPD, PGZIPA and PGZIPD polypeptides, useful for treating
PT   metabolic-related diseases or disorders, e.g. obesity, impaired glucose
PT   or insulin tolerance, atherosclerosis, heart diseases, hypertension or
PT   diabetes.
XX
PS   Disclosure; Page 122-123; 124pp; English.
XX
CC   The present invention relates to novel isoforms of Genset zinc-alpha-2-
CC   glycoprotein (ZAG) interacting protein (GZIP). The invention further
CC   relates to novel NGZIPA, NGZIPD, PGZIPA and PGZIPD proteins and their
CC   corresponding polynucleotides. Sequences of the invention are useful for
CC   reducing body mass, decreasing fat mass or increasing lean muscle mass,
CC   for treating metabolic-related diseases or disorders (e.g. obesity,
CC   impaired glucose tolerance, insulin tolerance, atherosclerosis, heart
CC   diseases, hypertension, stroke, type II diabetes) and glomerulonephritis,
CC   for controlling blood glucose and for improving insulin sensitivity. They
CC   are also useful in protein therapy. The present sequence is human APM1
CC   DNA used in the invention
XX
SQ   Sequence 735 BP; 179 A; 193 C; 202 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.38e-85      Length:          735
Score:                    708.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       8             Gaps:            0

US-10-072-159-11 (1-130) x AAD56155 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 6
ADC21966
ID   ADC21966 standard; DNA; 735 BP.
XX
AC   ADC21966;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human insulin resistance improving agent-related coding sequence.
XX
KW   insulin resistance improving agent; adiponectin C; leptin; obesity;
KW   cardiovascular diseases; diabetes; type II diabetes; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .735
FT                   /*tag=  a
FT                   /product= "Human insulin resistance improving agent-
FT                   related protein"
XX
PN   WO2003063894-A1.
XX
PD   07-AUG-2003.
XX
PF   26-JUL-2002; 2002WO-JP007599.
XX
PR   31-JAN-2002; 2002JP-00023554.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kadowaki T,  Yamauchi T,  Kamon J,  Waki H,  Nagai R,  Kimura S;
PI   Tomita M;
XX
DR   WPI; 2003-627572/59.
DR   P-PSDB; ADC21967.
XX
PT   Agents for improving fat-rich diet-induced insulin resistance containing
PT   C-terminal side spherical region of adiponectin C, adiponectin or their
PT   genes, applicable in treating obesity, heart diseases and diabetes.
XX
PS   Disclosure; SEQ ID NO 1; 46pp; Japanese.
XX
CC   The invention comprises agents for improving insulin resistance, the
CC   agents contain active ingredients, such as: C-terminal side spherical
CC   region of adiponectin C, adiponectin or their genes, and optionally
CC   leptin or its gene. The agents of the invention are applicable in
CC   treating: obesity, cardiovascular diseases, and diabetes - particularly
CC   type II diabetes. The present DNA sequence was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.38e-85      Length:          735
Score:                    708.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0

US-10-072-159-11 (1-130) x ADC21966 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582
```

```
Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 7
ADF16357
ID ADF16357 standard; DNA; 735 BP.
XX
AC ADF16357;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related DNA sequence SeqID1449.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040891.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
DR WPI; 2003-598517/56.
DR P-PSDB; ADF16683.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 1449; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC therapeutic protein which was fused with human albumin to create a novel
CC albumin fusion protein of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-85	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADF16357 (1-735)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 8
ADF16359
ID ADF16359 standard; DNA; 735 BP.
XX
AC ADF16359;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related DNA sequence SeqID1451.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX

```
PF   23-DEC-2002; 2002WO-US040891.
XX
PR   21-DEC-2001; 2001US-0341811P.
PR   24-JAN-2002; 2002US-0350358P.
PR   28-JAN-2002; 2002US-0351360P.
PR   26-FEB-2002; 2002US-0359370P.
PR   28-FEB-2002; 2002US-0360000P.
PR   27-MAR-2002; 2002US-0367500P.
PR   08-APR-2002; 2002US-0370227P.
PR   10-MAY-2002; 2002US-0378950P.
PR   24-MAY-2002; 2002US-0382617P.
PR   28-MAY-2002; 2002US-0383123P.
PR   05-JUN-2002; 2002US-0385708P.
PR   10-JUL-2002; 2002US-0394625P.
PR   24-JUL-2002; 2002US-0398008P.
PR   09-AUG-2002; 2002US-0402131P.
PR   13-AUG-2002; 2002US-0402708P.
PR   18-SEP-2002; 2002US-0411355P.
PR   18-SEP-2002; 2002US-0411426P.
PR   02-OCT-2002; 2002US-0414984P.
PR   11-OCT-2002; 2002US-0417611P.
PR   23-OCT-2002; 2002US-0420246P.
PR   05-NOV-2002; 2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA   (PRIN-) PRINCIPIA PHARM CORP.
XX
PI   Ballance DJ,  Turner AJ,  Rosen CA,  Haseltine WA;
XX
DR   WPI; 2003-598517/56.
DR   P-PSDB; ADF16685.
XX
PT   New albumin fusion protein, useful for preparing a composition for
PT   treating diabetes mellitus.
XX
PS   Example 4; SEQ ID NO 1451; 24pp; English.
XX
CC   This invention relates to a novel albumin fusion protein having albumin
CC   or biological activity. Human serum albumin is responsible for a
CC   significant proportion of the osmotic pressure of serum and also
CC   functions as a carrier of endogenous and exogenous ligands. The fusion of
CC   albumin to a therapeutic protein may increase shelf-life and stability of
CC   the therapeutic protein. The albumin fusion protein of the invention may
CC   allow production of compositions with antidiabetic activity whilst the
CC   nucleotide sequence which encodes it may be useful for gene therapy. The
CC   albumin fusion protein is useful for preparing a composition for treating
CC   diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC   therapeutic protein which was fused with human albumin to create a novel
CC   albumin fusion protein of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/publishedpct_sequences
XX
SQ   Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.38e-85        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-072-159-11 (1-130) x ADF16359 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 9
ADF16358
ID   ADF16358 standard; DNA; 735 BP.
XX
AC   ADF16358;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human albumin fusion protein-related DNA sequence SeqID1450.
XX
KW   albumin fusion protein; albumin activity; human serum albumin;
KW   serum osmotic pressure; shelf-life; stability; antidiabetic;
KW   gene therapy; diabetes mellitus; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003060071-A2.
XX
PD   24-JUL-2003.
XX
PF   23-DEC-2002; 2002WO-US040891.
XX
PR   21-DEC-2001; 2001US-0341811P.
PR   24-JAN-2002; 2002US-0350358P.
PR   28-JAN-2002; 2002US-0351360P.
PR   26-FEB-2002; 2002US-0359370P.
PR   28-FEB-2002; 2002US-0360000P.
PR   27-MAR-2002; 2002US-0367500P.
PR   08-APR-2002; 2002US-0370227P.
PR   10-MAY-2002; 2002US-0378950P.
PR   24-MAY-2002; 2002US-0382617P.
PR   28-MAY-2002; 2002US-0383123P.
PR   05-JUN-2002; 2002US-0385708P.
PR   10-JUL-2002; 2002US-0394625P.
PR   24-JUL-2002; 2002US-0398008P.
PR   09-AUG-2002; 2002US-0402131P.
PR   13-AUG-2002; 2002US-0402708P.
PR   18-SEP-2002; 2002US-0411355P.
PR   18-SEP-2002; 2002US-0411426P.
PR   02-OCT-2002; 2002US-0414984P.
PR   11-OCT-2002; 2002US-0417611P.
PR   23-OCT-2002; 2002US-0420246P.
PR   05-NOV-2002; 2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA   (PRIN-) PRINCIPIA PHARM CORP.
XX
PI   Ballance DJ,  Turner AJ,  Rosen CA,  Haseltine WA;
XX
DR   WPI; 2003-598517/56.
DR   P-PSDB; ADF16684.
```

XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 1450; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC therapeutic protein which was fused with human albumin to create a novel
CC albumin fusion protein of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-85	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADF16358 (1-735)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 10
ADE93611
ID ADE93611 standard; cDNA; 735 BP.
XX
AC ADE93611;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(1-244) cDNA.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
KW wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX
DR WPI; 2003-598262/56.
DR P-PSDB; ADE93603.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Disclosure; SEQ ID NO 9; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 cDNA of the
CC invention.
XX
SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-85	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADE93611 (1-735)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402
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Qy          21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy          41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy          61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy          81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy         101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy         121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
               |||||||||||||||||||||||||||||
Db         703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 11
ADH21732
ID ADH21732 standard; DNA; 735 BP.
XX
AC ADH21732;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human adiponectin-encoding DNA, SEQ ID NO:529.
XX
KW Fusion protein; human serum albumin; HSA; therapeutic protein;
KW shelf-life; in vitro biological activity; in vivo biological activity;
KW metabolic disorder; endocrine disorder; diabetes; type 1; type 2;
KW diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;
KW retinopathy; cardiovascular disorder; heart disease; renal disorder;
KW obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;
KW anorectic; ophthalmological; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003059934-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040892.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Haseltine WA;
XX
DR WPI; 2003-598501/56.
DR P-PSDB; ADH21884.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Disclosure; SEQ ID NO 529; 1086pp; English.
XX
CC The invention relates to fusion proteins comprising human serum albumin
CC (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,
CC antibody or peptide or their variants or fragments. The therapeutic
CC protein may be fused to the N-terminus, the C-terminus or both termini of
CC albumin via a linker. The albumin component of the fusion proteins
CC prolongs the shelf-life and the in vitro and vivo biological activity of
CC the proteins compared with those of the corresponding therapeutic
CC proteins on their own. The invention also relates to nucleic acids
CC encoding albumin fusion proteins, vectors and host cells comprising an
CC albumin fusion protein nucleic acid, compositions and kits comprising an
CC albumin fusion protein, the method of extending the shelf-life of a
CC therapeutic protein by fusion with albumin, and the treatment of disease
CC using an albumin fusion protein. The albumin fusion proteins may be used
CC in the treatment of metabolic/endocrine disorders, diabetes and diabetes-
CC related conditions. Specifically the albumin fusion proteins may be used
CC to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders
CC (especially neuropathy), retinopathy, cardiovascular disorders
CC (especially heart disease, renal disorders and obesity. The proteins may
CC also be used in a method of maintaining a basal glucose level in a
CC patient and in a method for losing weight. The present sequence is
CC related to the invention.
XX
SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-85	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-072-159-11 (1-130) x ADH21732 (1-735)

```
Qy           1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy          21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy          41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy          61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy          81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy         101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy         121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
               |||||||||||||||||||||||||||||
Db         703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 12
ADH21734
ID ADH21734 standard; DNA; 735 BP.
XX
AC ADH21734;

```
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human HDALV07-encoding DNA, SEQ ID NO:531.
XX
KW   Fusion protein; human serum albumin; HSA; therapeutic protein;
KW   shelf-life; in vitro biological activity; in vivo biological activity;
KW   metabolic disorder; endocrine disorder; diabetes; type 1; type 2;
KW   diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;
KW   retinopathy; cardiovascular disorder; heart disease; renal disorder;
KW   obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;
KW   anorectic; ophthalmological; gene therapy; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003059934-A2.
XX
PD   24-JUL-2003.
XX
PF   23-DEC-2002; 2002WO-US040892.
XX
PR   21-DEC-2001; 2001US-0341811P.
PR   24-JAN-2002; 2002US-0350358P.
PR   26-FEB-2002; 2002US-0359370P.
PR   28-FEB-2002; 2002US-0360000P.
PR   27-MAR-2002; 2002US-0367500P.
PR   08-APR-2002; 2002US-0370227P.
PR   10-MAY-2002; 2002US-0378950P.
PR   24-JUL-2002; 2002US-0398008P.
PR   09-AUG-2002; 2002US-0402131P.
PR   13-AUG-2002; 2002US-0402708P.
PR   18-SEP-2002; 2002US-0411355P.
PR   02-OCT-2002; 2002US-0414984P.
PR   11-OCT-2002; 2002US-0417611P.
PR   23-OCT-2002; 2002US-0420246P.
PR   05-NOV-2002; 2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2003-598501/56.
DR   P-PSDB; ADH21886.
XX
PT   New albumin fusion protein, useful for preparing a composition for
PT   treating diabetes mellitus.
XX
PS   Disclosure; SEQ ID NO 531; 1086pp; English.
XX
CC   The invention relates to fusion proteins comprising human serum albumin
CC   (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,
CC   antibody or peptide or their variants or fragments. The therapeutic
CC   protein may be fused to the N-terminus, the C-terminus or both termini of
CC   albumin via a linker. The albumin component of the fusion proteins
CC   prolongs the shelf-life and the in vitro and vivo biological activity of
CC   the proteins compared with those of the corresponding therapeutic
CC   proteins on their own. The invention also relates to nucleic acids
CC   encoding albumin fusion proteins, vectors and host cells comprising an
CC   albumin fusion protein nucleic acid, compositions and kits comprising an
CC   albumin fusion protein, the method of extending the shelf-life of a
CC   therapeutic protein by fusion with albumin, and the treatment of disease
CC   using an albumin fusion protein. The albumin fusion proteins may be used
CC   in the treatment of metabolic/endocrine disorders, diabetes and diabetes-
CC   related conditions. Specifically the albumin fusion proteins may be used
CC   to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders
CC   (especially neuropathy), retinopathy, cardiovascular disorders
CC   (especially heart disease, renal disorders and obesity. The proteins may
CC   also be used in a method of maintaining a basal glucose level in a
CC   patient and in a method for losing weight. The present sequence is
CC   related to the invention.
XX
SQ   Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.:              1.38e-85        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-072-159-11 (1-130) x ADH21734 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

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RESULT 13
ADH21733
ID   ADH21733 standard; DNA; 735 BP.
XX
AC   ADH21733;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human HDALV07(GD)/adiponectin-encoding DNA, SEQ ID NO:530.
XX
KW   Fusion protein; human serum albumin; HSA; therapeutic protein;
KW   shelf-life; in vitro biological activity; in vivo biological activity;
KW   metabolic disorder; endocrine disorder; diabetes; type 1; type 2;
KW   diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;
KW   retinopathy; cardiovascular disorder; heart disease; renal disorder;
KW   obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;
KW   anorectic; ophthalmological; gene therapy; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003059934-A2.
XX
PD   24-JUL-2003.
XX
PF   23-DEC-2002; 2002WO-US040892.
XX
PR   21-DEC-2001; 2001US-0341811P.
PR   24-JAN-2002; 2002US-0350358P.
PR   26-FEB-2002; 2002US-0359370P.
PR   28-FEB-2002; 2002US-0360000P.
PR   27-MAR-2002; 2002US-0367500P.
PR   08-APR-2002; 2002US-0370227P.
PR   10-MAY-2002; 2002US-0378950P.
PR   24-JUL-2002; 2002US-0398008P.
PR   09-AUG-2002; 2002US-0402131P.
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PR   13-AUG-2002; 2002US-0402708P.
PR   18-SEP-2002; 2002US-0411355P.
PR   02-OCT-2002; 2002US-0414984P.
PR   11-OCT-2002; 2002US-0417611P.
PR   23-OCT-2002; 2002US-0420246P.
PR   05-NOV-2002; 2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2003-598501/56.
DR   P-PSDB; ADH21885.
XX
PT   New albumin fusion protein, useful for preparing a composition for
PT   treating diabetes mellitus.
XX
PS   Disclosure; SEQ ID NO 530; 1086pp; English.
XX
CC   The invention relates to fusion proteins comprising human serum albumin
CC   (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,
CC   antibody or peptide or their variants or fragments. The therapeutic
CC   protein may be fused to the N-terminus, the C-terminus or both termini of
CC   albumin via a linker. The albumin component of the fusion proteins
CC   prolongs the shelf-life and the in vitro and vivo biological activity of
CC   the proteins compared with those of the corresponding therapeutic
CC   proteins on their own. The invention also relates to nucleic acids
CC   encoding albumin fusion proteins, vectors and host cells comprising an
CC   albumin fusion protein nucleic acid, compositions and kits comprising an
CC   albumin fusion protein, the method of extending the shelf-life of a
CC   therapeutic protein by fusion with albumin, and the treatment of disease
CC   using an albumin fusion protein. The albumin fusion proteins may be used
CC   in the treatment of metabolic/endocrine disorders, diabetes and diabetes-
CC   related conditions. Specifically the albumin fusion proteins may be used
CC   to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders
CC   (especially neuropathy), retinopathy, cardiovascular disorders
CC   (especially heart disease, renal disorders and obesity. The proteins may
CC   also be used in a method of maintaining a basal glucose level in a
CC   patient and in a method for losing weight. The present sequence is
CC   related to the invention.
XX
SQ   Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.38e-85        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-072-159-11 (1-130) x ADH21733 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 14
ADF14853
ID   ADF14853 standard; DNA; 735 BP.
XX
AC   ADF14853;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human arteriosclerosis-related protein coding sequence, SEQ ID 1.
XX
KW   Arteriosclerosis; adiponectin; scavenger receptor A ;
KW   antiarteriosclerotic; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .735
FT                   /*tag= a
FT                   /product= "Human arteriosclerosis-related protein"
XX
PN   WO2003099319-A1.
XX
PD   04-DEC-2003.
XX
PF   26-MAY-2003; 2003WO-JP006518.
XX
PR   24-MAY-2002; 2002JP-00151220.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kadowaki T,  Yamauchi T,  Kubota N,  Terauchi Y,  Kubota T,  Noda T;
PI   Nagai R,  Imai Y;
XX
DR   WPI; 2004-023231/02.
DR   P-PSDB; ADF14854.
XX
PT   Preventives or remedies for arteriosclerosis containing agents for
PT   regulating scavenger receptor A expression in arterial walls to inhibit
PT   lipid accumulation in microphages and to prevent its onset and
PT   progression.
XX
PS   Disclosure; SEQ ID NO 1; 46pp; Japanese.
XX
CC   The present invention relates to preventives or remedies for
CC   arteriosclerosis, which contain as active ingredient a spherical region
CC   in the C-terminal side of adiponectin, adiponectin or their gene. Such
CC   drugs contain agents for regulating scavenger receptor A expression in
CC   arterial wall to inhibit lipid accumulation in microphages and to prevent
CC   onset and progression of arteriosclerosis with direct stoppage of
CC   endangium form thickening. The present sequence was used to illustrate
CC   the invention.
XX
SQ   Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.38e-85        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     12              Gaps:           0

US-10-072-159-11 (1-130) x ADF14853 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
                ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 15
ADD93529
ID   ADD93529 standard; cDNA; 742 BP.
XX
AC   ADD93529;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel nucleic acid NOV2e, homologous to human adiponectin.
XX
KW   NOV2e; human; adiponectin; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             11. .712
FT                   /*tag= a
FT                   /partial
FT                   /product= "Human NOV2e"
FT                   /note= "No start codon"
XX
PN   WO2003078572-A2.
XX
PD   25-SEP-2003.
XX
PF   06-MAR-2003; 2003WO-US006859.
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PR   15-MAR-2002; 2002US-0365034P.
PR   19-MAR-2002; 2002US-0365477P.
PR   21-MAR-2002; 2002US-0366420P.
PR   05-MAR-2003; 2003US-00379747.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Chant JS,  Chaudhuri A,  Edinger SR,  Gangolli EA;
PI   Malyankar UM,  Miller CE,  Ooi CE,  Ort T,  Patturajan M,  Rastelli L;
PI   Rieger DK,  Shimkets RA,  Zerhusen BD;
XX
DR   WPI; 2003-779122/73.
DR   P-PSDB; ADD93530.
XX
PT   New isolated NOVX polypeptides and polynucleotides, useful for
PT   preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT   osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT   asthma, or infections.
XX
PS   Claim 20; Page 108; 205pp; English.
XX
CC   The present sequence is that of a novel polynucleotide encoding novel
CC   NOV2e, a polypeptide that shows amino acid sequence homology to the human
CC   adiponectin (adipose most abundant gene transcript 1, APM1). The
CC   adiponectin gene is the most abundant gene transcript in adipose cells
CC   that regulates lipid metabolism. An interaction between adiponectin and
CC   calcium modulating ligand was identified, indicating a novel pathway by
CC   which adiponectin may induce lipid breakdown in muscle cells and
CC   adipocytes. The invention is based on the identification of proteins and
CC   polypeptides, and the nucleic acids encoding them, that are
CC   differentially modulated in a pathological state, disease or an abnormal
CC   condition or state. These are targets for therapeutic agents and can be
CC   used in screening methodologies to identify candidate therapeutic agents
CC   which interact with the target and thereby exert a desired or favourable
CC   effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
CC   haematopoiesis, wound healing and angiogenesis. Methods for diagnosis,
CC   treatment and prevention of disorders involving the novel human nucleic
CC   acids and proteins are provided. The nucleic acids are further used in
CC   gene therapy, as hybridization probes and primers, in chromosome mapping,
CC   tissue typing, preventive medicine, and pharmacogenomics.
XX
SQ   Sequence 742 BP; 189 A; 204 C; 197 G; 152 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.4e-85        Length:          742
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       10             Gaps:            0

US-10-072-159-11 (1-130) x ADD93529 (1-742)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        320 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 379

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 439

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 499

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 559

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 619

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 679

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        680 ACAGGCTTTCTTCTCTACCATGACACCAAC 709


Search completed: December 3, 2004, 11:01:11
Job time : 405 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:58:48 ; Search time 2353 Seconds
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Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708	100.0	492	6	AX800356	AX800356 Sequence
2	708	100.0	521	9	HSA131461	AJ131461 Homo sapi
3	708	100.0	537	6	AX800405	AX800405 Sequence
4	708	100.0	564	6	AX800355	AX800355 Sequence
5	708	100.0	582	6	AX800354	AX800354 Sequence
6	708	100.0	735	6	AX752056	AX752056 Sequence
7	708	100.0	735	6	AX800349	AX800349 Sequence
8	708	100.0	1313	6	AR034253	AR034253 Sequence
9	708	100.0	4510	6	CQ715267	CQ715267 Sequence
10	708	100.0	4517	6	AR138194	AR138194 Sequence
11	708	100.0	4517	6	AR255755	AR255755 Sequence
12	708	100.0	4517	6	AR337311	AR337311 Sequence
13	708	100.0	4517	6	AR343651	AR343651 Sequence
14	708	100.0	4517	6	AX195211	AX195211 Sequence
15	708	100.0	4517	6	AX335029	AX335029 Sequence
16	708	100.0	4517	6	AX358521	AX358521 Sequence
17	708	100.0	4517	6	AX767959	AX767959 Sequence
18	708	100.0	4517	6	AX951629	AX951629 Sequence
19	708	100.0	4517	6	AX960544	AX960544 Sequence
20	708	100.0	4517	6	BD074783	BD074783 Homolog o
21	708	100.0	4517	9	HUMUPST2	D45371 Human apM1
22	708	100.0	4537	9	AB012163S3	AB012165 Homo sapi
23	708	100.0	4545	6	BD238086	BD238086 Genome se
24	708	100.0	4545	6	AR344520	AR344520 Sequence
25	708	100.0	4545	6	AX134174	AX134174 Sequence
26	708	100.0	13001	9	AC072018	AC072018 Homo sapi
27	708	100.0	20966	6	BD238082	BD238082 Genome se
28	708	100.0	20966	6	AR337312	AR337312 Sequence
29	708	100.0	20966	6	AR343652	AR343652 Sequence
30	708	100.0	20966	6	AR344516	AR344516 Sequence
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33	708	100.0	20966	6	AX358523	AX358523 Sequence
34	708	100.0	20966	6	AX767961	AX767961 Sequence
35	708	100.0	20966	6	AX960548	AX960548 Sequence
36	708	100.0	176155	2	AC012149	AC012149 Homo sapi
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40	703	99.3	537	6	AX800408	AX800408 Sequence
41	702	99.2	537	6	AX800402	AX800402 Sequence
42	702	99.2	537	6	AX800404	AX800404 Sequence
43	700	98.9	537	6	AX800407	AX800407 Sequence
44	699	98.7	537	6	AX800406	AX800406 Sequence
45	699	98.7	537	6	AX800409	AX800409 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX800356 492 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 16 from Patent WO03055916.
ACCESSION AX800356
VERSION AX800356.1 GI:37653576
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
Halkier,T. and Bogsnes,A.
TITLE Adiponectin fragments and conjugates
JOURNAL Patent: WO 03055916-A 16 10-JUL-2003;
Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
(Cayman) Limited (KY)
FEATURES Location/Qualifiers
source 1..492
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="apM1(82-244) coding sequence"
ORIGIN

Alignment Scores:
Pred. No.: 2.42e-74 Length: 492

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Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-072-159-11 (1-130) x AX800356 (1-492)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 219

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        220 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 279

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Db        280 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 339

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        340 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 399

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 459

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        460 ACAGGCTTTCTTCTCTACCATGACACCAAC 489

RESULT 2
HSA131461
LOCUS       HSA131461               521 bp    DNA     linear   PRI 21-OCT-1999
DEFINITION  Homo sapiens apM-1 gene, exon 3.
ACCESSION   AJ131461
VERSION     AJ131461.1  GI:5725240
KEYWORDS    adipocyte-specific secretory protein; APM-1 gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schaffler,A., Orso,E., Palitzsch,K.D., Buchler,C., Drobnik,W.,
            Furst,A., Scholmerich,J. and Schmitz,G.
  TITLE     The human apM-1, an adipocyte-specific gene linked to the family of
            TNF's and to genes expressed in activated T cells, is mapped to
            chromosome 1q21.3-q23, a susceptibility locus identified for
            familial combined hyperlipidaemia (FCH)
  JOURNAL   Biochem. Biophys. Res. Commun. 260 (2), 416-425 (1999)
  MEDLINE   99333693
   PUBMED   10403784
REFERENCE   2  (bases 1 to 521)
  AUTHORS   Schaeffler,A.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-DEC-1998) Schaeffler A.J., University of Regensburg,
            Germany, Institute for Clinical Chemistry and Laboratory Medicine,
            Franz-Josef-Strauss-Allee 11, D-93042, GERMANY
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q21.3-q23"
     gene            1. .521
                     /gene="apM-1"
     exon            1. .>521
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ORIGIN

Alignment Scores:
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Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-072-159-11 (1-130) x HSA131461 (1-521)

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Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 248

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 308

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 368

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        369 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 428

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        429 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 488

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        489 ACAGGCTTTCTTCTCTACCATGACACCAAC 518

RESULT 3
AX800405
LOCUS       AX800405                537 bp    DNA     linear   PAT 13-OCT-2003
DEFINITION  Sequence 65 from Patent WO03055916.
ACCESSION   AX800405
VERSION     AX800405.1  GI:37653580
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rasmussen,P.B:, Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
            Halkier,T. and Bogsnes,A.
  TITLE     Adiponectin fragments and conjugates
  JOURNAL   Patent: WO 03055916-A 65 10-JUL-2003;
            Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
            (Cayman) Limited (KY)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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ORIGIN

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Score:                  708.00          Matches:        130
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Best Local Similarity:  100.00%         Mismatches:     0
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Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-10-072-159-11 (1-130) x AX800405 (1-537)

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Db        145 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 204

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        205 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 264

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 324

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        445 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 504

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        505 ACAGGCTTTCTTCTCTACCATGACACCAAC 534

RESULT 4
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LOCUS       AX800355                564 bp    DNA     linear   PAT 13-OCT-2003
DEFINITION  Sequence 15 from Patent WO03055916.
ACCESSION   AX800355
VERSION     AX800355.1  GI:37653575
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
            Halkier,T. and Bogsnes,A.
  TITLE     Adiponectin fragments and conjugates
  JOURNAL   Patent: WO 03055916-A 15 10-JUL-2003;
            Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
            (Cayman) Limited (KY)
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ORIGIN

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Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-10-072-159-11 (1-130) x AX800355 (1-564)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 231

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 291

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 351

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 411

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 471

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 531

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        532 ACAGGCTTTCTTCTCTACCATGACACCAAC 561

RESULT 5
AX800354
LOCUS       AX800354                582 bp    DNA     linear   PAT 13-OCT-2003
DEFINITION  Sequence 14 from Patent WO03055916.
ACCESSION   AX800354
VERSION     AX800354.1  GI:37653574
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
            Halkier,T. and Bogsnes,A.
  TITLE     Adiponectin fragments and conjugates
  JOURNAL   Patent: WO 03055916-A 14 10-JUL-2003;
            Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
            (Cayman) Limited (KY)
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="apM1(52-244) coding sequence"
ORIGIN

Alignment Scores:
Pred. No.:              2.95e-74      Length:        582
Score:                  708.00        Matches:       130
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-10-072-159-11 (1-130) x AX800354 (1-582)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 249

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 309

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 369

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Db        370 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 429

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 489

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 549

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
                ||||||||||||||||||||||||||||||
Db        550 ACAGGCTTTCTTCTCTACCATGACACCAAC 579

RESULT 6
AX752056
LOCUS       AX752056               735 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 21 from Patent WO03033534.
ACCESSION   AX752056
VERSION     AX752056.1  GI:32134172
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Scalia,A., Dialynas,D. and Briggs,K.
  TITLE     NGZIPA, NGZIPD, PGZIPA, and PGZIPD polynucleotides and polypeptides
            and uses thereof
  JOURNAL   Patent: WO 03033534-A 21 24-APR-2003;
            Genset S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .735
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD99168.1"
                     /db_xref="GI:32134173"
                     /translation="MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIP
                     GHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKG
                     EPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYF
                     AYHITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGE
                     GERNGLYADNDNDSTFTGFLLYHDTN"
ORIGIN

Alignment Scores:
Pred. No.:              3.88e-74        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-072-159-11 (1-130) x AX752056 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 7
AX800349
LOCUS       AX800349               735 bp    DNA     linear   PAT 13-OCT-2003
DEFINITION  Sequence 9 from Patent WO03055916.
ACCESSION   AX800349
VERSION     AX800349.1  GI:37653573
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
            Halkier,T. and Bogsnes,A.
  TITLE     Adiponectin fragments and conjugates
  JOURNAL   Patent: WO 03055916-A 9 10-JUL-2003;
            Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
            (Cayman) Limited (KY)
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="apM1(1-244) coding sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.88e-74        Length:         735
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-072-159-11 (1-130) x AX800349 (1-735)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702
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Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              |||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732

RESULT 8
AR034253
LOCUS       AR034253               1313 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5869330.
ACCESSION   AR034253
VERSION     AR034253.1  GI:5949858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1313)
  AUTHORS   Scherer,P.E. and Lodish,H.F.
  TITLE     DNA encoding a novel serum protein produced exclusively in
            adipocytes
  JOURNAL   Patent: US 5869330-A 6 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1313
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 7.68e-74        Length:          1313
Score:                     708.00          Matches:         130
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               100.00%         Indels:          0
DB:                        6               Gaps:            0

US-10-072-159-11 (1-130) x AR034253 (1-1313)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 474

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 534

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 594

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 654

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 714

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 774

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        775 ACAGGCTTTCTTCTCTACCATGACACCAAC 804

RESULT 9
CQ715267
LOCUS       CQ715267               4510 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1201 from Patent WO02068579.
ACCESSION   CQ715267
VERSION     CQ715267.1  GI:42276124
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1201 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .4510
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                 3.29e-73        Length:          4510
Score:                     708.00          Matches:         130
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               100.00%         Indels:          0
DB:                        6               Gaps:            0

US-10-072-159-11 (1-130) x CQ715267 (1-4510)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 417

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 477

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 537

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 597

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 657

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 717

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        718 ACAGGCTTTCTTCTCTACCATGACACCAAC 747

RESULT 10
AR138194
LOCUS       AR138194               4517 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 9 from patent US 6197930.
ACCESSION   AR138194
VERSION     AR138194.1  GI:14479703
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4517)
  AUTHORS   Sheppard,P.O. and Humes,J.M.
  TITLE     Adipocyte-specific protein homologs
  JOURNAL   Patent: US 6197930-A 9 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .4517
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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Alignment Scores:
Pred. No.:                3.3e-73        Length:          4517
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-072-159-11 (1-130) x AR138194 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 11
AR255755
LOCUS       AR255755                4517 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6482612.
ACCESSION   AR255755
VERSION     AR255755.1  GI:27304874
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4517)
  AUTHORS   Sheppard,P.O. and Humes,J.M.
  TITLE     Adipocyte-specific protein homologs
  JOURNAL   Patent: US 6482612-A 9 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .4517
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.3e-73        Length:          4517
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-072-159-11 (1-130) x AR255755 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 12
AR337311
LOCUS       AR337311                4517 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566332.
ACCESSION   AR337311
VERSION     AR337311.1  GI:33723295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4517)
  AUTHORS   Fruebis,J., Erickson,M.R., Yen,F. and Bihain,B.
  TITLE     OBG3 globular head and uses thereof for decreasing body mass
  JOURNAL   Patent: US 6566332-A 5 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .4517
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:                3.3e-73        Length:          4517
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-072-159-11 (1-130) x AR337311 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668
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Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 13
AR343651
LOCUS       AR343651               4517 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6579852.
ACCESSION   AR343651
VERSION     AR343651.1  GI:33739445
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4517)
  AUTHORS   Fruebis,J., Erickson,M.R., Yen-Potin,F. and Bihain,B.
  TITLE     OBG3 globular head and uses thereof for decreasing body mass
  JOURNAL   Patent: US 6579852-A 5 17-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .4517
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.3e-73        Length:          4517
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-072-159-11 (1-130) x AR343651 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 14
AX195211
LOCUS       AX195211               4517 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 5 from Patent WO0151645.
ACCESSION   AX195211
VERSION     AX195211.1  GI:15385772
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bihain,B., Erickson,M.R., Fruebis,J. and Yen-Potin,F.
  TITLE     Obg3 globular head and uses thereof for decreasing body mass
  JOURNAL   Patent: WO 0151645-A 5 19-JUL-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                3.3e-73        Length:          4517
Score:                    708.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-072-159-11 (1-130) x AX195211 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 15
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LOCUS       AX335029               4517 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 5538 from Patent WO0194629.
ACCESSION   AX335029
VERSION     AX335029.1  GI:18125748
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
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  JOURNAL   Patent: WO 0194629-A 5538 13-DEC-2001;
            Avalon Pharmaceuticals (US)
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              3.3e-73         Length:         4517
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
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US-10-072-159-11 (1-130) x AX335029 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758


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and is derived by analysis of the total score distribution.

SUMMARIES

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3	708	100.0	564	15	US-10-325-717-15	Sequence 15, Appl
4	708	100.0	582	15	US-10-325-717-14	Sequence 14, Appl
5	708	100.0	735	15	US-10-325-717-9	Sequence 9, Appli
6	708	100.0	742	16	US-10-379-747-13	Sequence 13, Appl
7	708	100.0	754	16	US-10-379-747-9	Sequence 9, Appli
8	708	100.0	778	16	US-10-379-747-11	Sequence 11, Appl
9	708	100.0	783	16	US-10-379-747-5	Sequence 5, Appli
10	708	100.0	1550	15	US-10-411-120-19	Sequence 19, Appl
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16	708	100.0	4517	15	US-10-197-293-9	Sequence 9, Appli
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37	655	92.5	1276	9	US-09-909-547-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-10-325-717-16
; Sequence 16, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogsnes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25

```
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;    LENGTH: 492
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: apM1(82-244) coding sequence
US-10-325-717-16

Alignment Scores:
Pred. No.:                1.24e-88        Length:         492
Score:                    708.00          Matches:        130
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       15              Gaps:           0

US-10-072-159-11 (1-130) x US-10-325-717-16 (1-492)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 159

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 219

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 279

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 339

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 399

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 459

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        460 ACAGGCTTTCTTCTCTACCATGACACCAAC 489

RESULT 2
US-10-325-717-65
; Sequence 65, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
;    LENGTH: 537
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic construct encoding Y111N-apM1(82-244)
US-10-325-717-65

Alignment Scores:
Pred. No.:                1.41e-88        Length:         537
Score:                    708.00          Matches:        130
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       15              Gaps:           0

US-10-072-159-11 (1-130) x US-10-325-717-65 (1-537)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 204

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 264

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 324

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 384

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 444

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 504

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        505 ACAGGCTTTCTTCTCTACCATGACACCAAC 534

RESULT 3
US-10-325-717-15
; Sequence 15, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
;  APPLICANT: Rasmussen, Poul Baad
;  APPLICANT:  Andersen, Kim Vilbour
;  APPLICANT:  Pedersen, Anders Hjelholt
;  APPLICANT:  Schambye, Hans Thalsgaard
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Bogsnes, Are
;  TITLE OF INVENTION: Adiponectin Fragments and Conjugates
;  FILE REFERENCE: 0251us610
;  CURRENT APPLICATION NUMBER: US/10/325,717
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/412,169
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/394,117
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/375,492
;  PRIOR FILING DATE: 2002-04-25
;  PRIOR APPLICATION NUMBER: US 60/343,482
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 15
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(58-244) coding sequence
US-10-325-717-15

Alignment Scores:

Pred. No.:	1.52e-88	Length:	564
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-072-159-11 (1-130) x US-10-325-717-15 (1-564)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 231

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 291

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 351

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 411

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 471

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 531

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        532 ACAGGCTTTCTTCTCTACCATGACACCAAC 561
```

RESULT 4
US-10-325-717-14
; Sequence 14, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogsnes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(52-244) coding sequence
US-10-325-717-14

Alignment Scores:

Pred. No.:	1.59e-88	Length:	582
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-072-159-11 (1-130) x US-10-325-717-14 (1-582)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 249

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 309

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 369

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 429

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 489

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 549

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        550 ACAGGCTTTCTTCTCTACCATGACACCAAC 579
```

RESULT 5
US-10-325-717-9
; Sequence 9, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogsnes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: apM1(1-244) coding sequence
US-10-325-717-9

Alignment Scores:

Pred. No.:	2.26e-88	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-072-159-11 (1-130) x US-10-325-717-9 (1-735)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 402

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 462

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 582

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        703 ACAGGCTTTCTTCTCTACCATGACACCAAC 732
```

RESULT 6
US-10-379-747-13
; Sequence 13, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Chant, John S.;
; APPLICANT: Chaudhuri, Amitabha ;
; APPLICANT: Edinger, Shlomit R.;
; APPLICANT: Gangolli, Esha A.;
; APPLICANT: Malyankar, Uriel M.;
; APPLICANT: Miller, Charles E.;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Ort, Tatiana A.;
; APPLICANT: Patturajan, Meera ;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568B
; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 13
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(709)
US-10-379-747-13

Alignment Scores:

Pred. No.:	2.29e-88	Length:	742
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-10-072-159-11 (1-130) x US-10-379-747-13 (1-742)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 379

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 439

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 499

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 559

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 619

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 679

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        680 ACAGGCTTTCTTCTCTACCATGACACCAAC 709
```

RESULT 7
US-10-379-747-9
; Sequence 9, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Chant, John S.;
; APPLICANT: Chaudhuri, Amitabha ;
; APPLICANT: Edinger, Shlomit R.;
; APPLICANT: Gangolli, Esha A.;
; APPLICANT: Malyankar, Uriel M.;
; APPLICANT: Miller, Charles E.;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Ort, Tatiana A.;
; APPLICANT: Patturajan, Meera ;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-568B
; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420

```
;  PRIOR FILING DATE: 2002-03-21
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 9
;   LENGTH: 754
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)..(745)
US-10-379-747-9

Alignment Scores:
Pred. No.:              2.35e-88        Length:         754
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     16              Gaps:           0

US-10-072-159-11 (1-130) x US-10-379-747-9 (1-754)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 415

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 475

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 535

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 595

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 655

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 715

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        716 ACAGGCTTTCTTCTCTACCATGACACCAAC 745

RESULT 8
US-10-379-747-11
; Sequence 11, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E.;
;  APPLICANT:  Chant, John S.;
;  APPLICANT:  Chaudhuri, Amitabha ;
;  APPLICANT:  Edinger, Shlomit R.;
;  APPLICANT:  Gangolli, Esha A.;
;  APPLICANT:  Malyankar, Uriel M.;
;  APPLICANT:  Miller, Charles E.;
;  APPLICANT:  Ooi, Chean Eng;
;  APPLICANT:  Ort, Tatiana A.;
;  APPLICANT:  Patturajan, Meera ;
;  APPLICANT:  Rastelli, Luca ;
;  APPLICANT:  Rieger, Daniel K.;
;  APPLICANT:  Shimkets, Richard A.;
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-568B
;  CURRENT APPLICATION NUMBER: US/10/379,747
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/365,034
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: 60/366,420
;  PRIOR FILING DATE: 2002-03-21
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 11
;   LENGTH: 778
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (17)..(766)
US-10-379-747-11

Alignment Scores:
Pred. No.:              2.46e-88        Length:         778
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     16              Gaps:           0

US-10-072-159-11 (1-130) x US-10-379-747-11 (1-778)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 436

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 496

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 556

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 616

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 676

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 736

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        737 ACAGGCTTTCTTCTCTACCATGACACCAAC 766

RESULT 9
US-10-379-747-5
; Sequence 5, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E.;
;  APPLICANT:  Chant, John S.;
;  APPLICANT:  Chaudhuri, Amitabha ;
;  APPLICANT:  Edinger, Shlomit R.;
;  APPLICANT:  Gangolli, Esha A.;
;  APPLICANT:  Malyankar, Uriel M.;
;  APPLICANT:  Miller, Charles E.;
;  APPLICANT:  Ooi, Chean Eng;
;  APPLICANT:  Ort, Tatiana A.;
;  APPLICANT:  Patturajan, Meera ;
;  APPLICANT:  Rastelli, Luca ;
```

```
;  APPLICANT:  Rieger, Daniel K.;
;  APPLICANT:  Shimkets, Richard A.;
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-568B
;  CURRENT APPLICATION NUMBER: US/10/379,747
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/365,034
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: 60/366,420
;  PRIOR FILING DATE: 2002-03-21
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 5
;   LENGTH: 783
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (12)..(743)
US-10-379-747-5

Alignment Scores:
Pred. No.:              2.49e-88        Length:         783
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     16              Gaps:           0

US-10-072-159-11 (1-130) x US-10-379-747-5 (1-783)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 413

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 473

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 533

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 593

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 653

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 713

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        714 ACAGGCTTTCTTCTCTACCATGACACCAAC 743

RESULT 10
US-10-411-120-19
; Sequence 19, Application US/10411120
; Publication No. US20030224425A1
; GENERAL INFORMATION:
;  APPLICANT: Blondel et al.
;  TITLE OF INVENTION: ACRP-30-like Polynucleotides, Polypeptides, and Antibodies
;  FILE REFERENCE: PT316P1
;  CURRENT APPLICATION NUMBER: US/10/411,120
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/328,419
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US02/32432
;  PRIOR FILING DATE: 2002-10-11
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 1550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1547)..(1547)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-411-120-19

Alignment Scores:
Pred. No.:              6.96e-88        Length:         1550
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     15              Gaps:           0

US-10-072-159-11 (1-130) x US-10-411-120-19 (1-1550)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 443

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 503

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 563

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 623

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 683

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 743

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        744 ACAGGCTTTCTTCTCTACCATGACACCAAC 773

RESULT 11
US-09-776-976-5
; Sequence 5, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
;  APPLICANT: Fruebis, Joachim
;  APPLICANT:  Erickson, Mary Ruth
;  APPLICANT:  Yen, Frances
;  APPLICANT:  Bihain, Bernard
;  TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
;  FILE REFERENCE: 76.US4.REG
;  CURRENT APPLICATION NUMBER: US/09/776,976
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/758,055
;  PRIOR FILING DATE: 2001-01-10
;  PRIOR APPLICATION NUMBER: US 60/176,228
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/198,087
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: US 60/299,881
```

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;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 4517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-776-976-5

Alignment Scores:
Pred. No.:              3.49e-87        Length:         4517
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-072-159-11 (1-130) x US-09-776-976-5 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 12
US-09-758-055-5
; Sequence 5, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
;  APPLICANT: Fruebis, Joachim
;  APPLICANT:  Erickson, Mary Ruth
;  APPLICANT:  Yen, Frances
;  APPLICANT:  Bihain, Bernard
;  TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
;  FILE REFERENCE: 76.US4.REG
;  CURRENT APPLICATION NUMBER: US/09/758,055
;  CURRENT FILING DATE:  2001-01-10
;  PRIOR APPLICATION NUMBER: US 60/176,228
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/198,087
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: US 60/299,881
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 4517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-758-055-5

Alignment Scores:
Pred. No.:              3.49e-87        Length:         4517
Score:                  708.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-072-159-11 (1-130) x US-09-758-055-5 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 13
US-09-909-547-5
; Sequence 5, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
;  APPLICANT: Fruebis, Joachim
;  APPLICANT:  Erickson, Mary Ruth
;  APPLICANT:  Yen, Frances
;  APPLICANT:  Bihain, Bernard
;  TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
;  FILE REFERENCE: 76.US6.CIP
;  CURRENT APPLICATION NUMBER: US/09/909,547
;  CURRENT FILING DATE:  2001-07-19
;  PRIOR APPLICATION NUMBER: US 09/776,976
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/758,055
;  PRIOR FILING DATE: 2001-01-10
;  PRIOR APPLICATION NUMBER: US 60/299,881
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: US 60/198,087
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: US 60/176,228
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 4517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-909-547-5

Alignment Scores:
Pred. No.:              3.49e-87        Length:         4517
Score:                  708.00          Matches:        130
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     9              Gaps:          0

US-10-072-159-11 (1-130) x US-09-909-547-5 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 14
US-09-964-824A-235
; Sequence 235, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
;  APPLICANT: Horrigan, Stephen
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-73
;  CURRENT APPLICATION NUMBER: US/09/964,824A
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: US/60/236,033
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,032
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,028
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 583
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
;   LENGTH: 4517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-824A-235

Alignment Scores:
Pred. No.:              3.49e-87       Length:        4517
Score:                  708.00         Matches:       130
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     9              Gaps:          0

US-10-072-159-11 (1-130) x US-09-964-824A-235 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758

RESULT 15
US-10-231-814-5
; Sequence 5, Application US/10231814
; Publication No. US20030100500A1
; GENERAL INFORMATION:
;  APPLICANT: Fruebis, Joachim
;  APPLICANT:  Erickson, Mary Ruth
;  APPLICANT:  Yen, Frances
;  APPLICANT:  Bihain, Bernard
;  TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
;  FILE REFERENCE: 76.US4.REG
;  CURRENT APPLICATION NUMBER: US/10/231,814
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: US/09/758,055
;  PRIOR FILING DATE: 2001-01-10
;  PRIOR APPLICATION NUMBER: US 60/176,228
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/198,087
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: US 60/299,881
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 4517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-231-814-5

Alignment Scores:
Pred. No.:              3.49e-87       Length:        4517
Score:                  708.00         Matches:       130
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     15             Gaps:          0

US-10-072-159-11 (1-130) x US-10-231-814-5 (1-4517)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 428

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 488

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 608

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 668

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 728

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
               ||||||||||||||||||||||||||||||
Db        729 ACAGGCTTTCTTCTCTACCATGACACCAAC 758
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Search completed: December 3, 2004, 12:38:49
Job time : 401 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:59:48 ; Search time 2971 Seconds
(without alignments)
1594.468 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10072159/runat_02122004_142305_15575/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10072159_@CGN_1_1_5180_@runat_02122004_142305_15575 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	708	100.0	1842	3	BC054496	BC054496 Homo sapi
c	2	708	100.0	3591	3	BC036509	BC036509 Homo sapi
	3	661	93.4	610	2	AW915595	AW915595 EST346899
	4	661	93.4	857	7	CO389083	CO389083 AGENCOURT
	5	655	92.5	523	5	BX519230	BX519230 BX519230
	6	655	92.5	552	2	BE625509	BE625509 uu19e06.y
	7	655	92.5	566	1	AA028544	AA028544 mi18b08.r
	8	655	92.5	921	3	AK003138	AK003138 Mus muscu
	9	655	92.5	1158	3	AK041214	AK041214 Mus muscu
c	10	652	92.1	605	4	BM384395	BM384395 UI-R-CN1-
	11	647	91.4	545	1	AI158610	AI158610 ud29f07.r
	12	638	90.1	1465	3	BC078720	BC078720 Rattus no
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c	14	636	89.8	577	5	BQ189822	BQ189822 UI-R-CN1-
	15	634	89.5	811	1	AA763396	AA763396 vw53g11.r
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	17	609	86.0	921	1	AA673154	AA673154 ve40g07.r
	18	604	85.3	508	1	AA493090	AA493090 vi71g11.r
	19	582	82.2	885	1	AI323115	AI323115 mj87e03.y
	20	574	81.1	856	5	BQ876848	BQ876848 AGENCOURT
	21	568	80.2	491	7	CF931240	CF931240 CF--06-R-
c	22	568	80.2	830	7	CK849149	CK849149 972010 BA
	23	558	78.8	468	2	AW988554	AW988554 ug08h07.y
	24	558	78.8	634	7	CO384703	CO384703 AGENCOURT
c	25	556	78.5	600	1	AA960123	AA960123 ub54f07.s
	26	555	78.4	694	2	BB225356	BB225356 BB225356
	27	551	77.8	786	7	CO400150	CO400150 AGENCOURT
	28	549	77.5	438	1	AA061943	AA061943 mj82d06.r
c	29	548	77.4	486	2	BE626169	BE626169 ut83f01.x
c	30	544.5	76.9	585	1	AI323469	AI323469 mj87e03.x
	31	537	75.8	468	2	AW911832	AW911832 uf39d11.y
	32	537	75.8	470	2	AW986727	AW986727 uf87a04.y
	33	537	75.8	519	2	BE478076	BE478076 162149 BA
	34	533	75.3	707	4	BG872725	BG872725 602793813
c	35	510	72.0	433	1	AI407605	AI407605 EST235895
	36	501	70.8	758	6	CF345349	CF345349 AGENCOURT
c	37	501	70.8	787	6	CF345350	CF345350 AGENCOURT
c	38	496	70.1	445	1	AI171410	AI171410 EST217370
	39	492	69.5	867	7	CF376220	CF376220 AGENCOURT
	40	490	69.2	406	4	BG090627	BG090627 mac09a09.
	41	475.5	67.2	766	7	CO387981	CO387981 AGENCOURT
	42	470	66.4	811	7	CK794688	CK794688 AGENCOURT
c	43	467.5	66.0	825	1	AI645984	AI645984 vw53g11.x
	44	462	65.3	625	1	AA451292	AA451292 vf84a04.r
	45	457	64.5	698	5	BX862914	BX862914 BX862914

ALIGNMENTS

RESULT 1
BC054496
LOCUS BC054496 1842 bp mRNA linear HTC 02-MAR-2004
DEFINITION Homo sapiens adipocyte, C1Q and collagen domain containing, mRNA (cDNA clone IMAGE:6192794), with apparent retained intron.
ACCESSION BC054496
VERSION BC054496.1 GI:32493391
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1842)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1842)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 98 Row: m Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4757759
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1842
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6192794"
                     /tissue_type="Peripheral Nervous System, sympathetic
                     trunk"
                     /clone_lib="Lupski_sympathetic_trunk"
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                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:                5.74e-80        Length:         1842
Score:                    708.00          Matches:        130
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-10-072-159-11 (1-130) x BC054496 (1-1842)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 427

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 487

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 547

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 607

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 667

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        668 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 727

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        728 ACAGGCTTTCTTCTCTACCATGACACCAAC 757

RESULT 2
BC036509/c
LOCUS       BC036509              3591 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5266441, mRNA.
ACCESSION   BC036509
VERSION     BC036509.1  GI:23242690
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3591)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 73 Row: o Column: 22
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="Testis"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
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ORIGIN

Alignment Scores:
Pred. No.:                1.34e-79        Length:         3591
Score:                    708.00          Matches:        130
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-10-072-159-11 (1-130) x BC036509 (1-3591)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAG 1889

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT 1829

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db       1828 CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 1769

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 CTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG 1709

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 1649

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 1589

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db       1588 ACAGGCTTTCTTCTCTACCATGACACCAAC 1559

RESULT 3
AW915595
LOCUS       AW915595                610 bp    mRNA    linear   EST 25-MAY-2000
DEFINITION  EST346899 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
            RGICY17 5' end, mRNA sequence.
ACCESSION   AW915595
VERSION     AW915595.1  GI:8081296
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            This clone is available through the ATCC, contact the ATCC
            tel#703-365-2700 for further information
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /clone="RGICY17"
                     /dev_stage="embryo 8, 12, 18 dpc"
                     /clone_lib="Normalized rat embryo, Bento Soares"
                     /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
ORIGIN

Alignment Scores:
Pred. No.:              1.59e-74        Length:         610
Score:                  661.00          Matches:        120
Percent Similarity:     96.92%          Conservative:   6
Best Local Similarity:  92.31%          Mismatches:     4
Query Match:            93.36%          Indels:         0
DB:                     2               Gaps:           0

US-10-072-159-11 (1-130) x AW915595 (1-610)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||  |||||||:::|||||||:::||||||||||||||||||
Db         58 TTCAGCGTAGGGCTGGAGACCCGCGTCACTGTCCCCAATGTTCCCATTCGCTTTACTAAG 117

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        118 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATT 177

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        178 CCGGGGCTCTACTACTTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGC 237

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||:::|||||||||||||||||||||||||||||    ||||||
Db        238 CTCTTCAAGAAGGACAAGGGCGTTCTCTTCACCTACGACCAGTATCAGGAAAAAAATGTG 297

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        298 GACCAGGCCTCTCGCTCCATGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAA 357

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||:::   ||||||||||||||||||    ||||||||||||||||||
Db        358 GTGTATGGGGAAGGGGACAACAATGGACTCTATGCAGATAATGTCAATGACTCTACATTT 417

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        418 ACAGGCTTCCTTCTCTACCATGATACCAAC 447

RESULT 4
CO389083
LOCUS       CO389083                857 bp    mRNA    linear   EST 30-JUN-2004
DEFINITION  AGENCOURT_26621565 NIH_MGC_253 Rattus norvegicus cDNA clone
            IMAGE:7304566 5', mRNA sequence.
ACCESSION   CO389083
VERSION     CO389083.1  GI:49496674
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
            College of Wisconsin
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15341  row: f  column: 20
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
     source          1. .857
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7304566"
                     /tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks.
                     Tissues were snap-frozen and transfered in -70c. RNAse
                     free the entire procedure."
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_253"
                     /note="Organ: ovary; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from female animals at 8 wk
                     old. Tissues were snap-frozen and kept at -80C for two
                     days before RNA extraction and purification (Tri-reagent
                     method). cDNA was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
                     resulted in an average insert size of 1.5 kb. This primary
```

library is normalized (non-normalized primary library is NIH_MGC_252) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	2.45e-74	Length:	857
Score:	661.00	Matches:	120
Percent Similarity:	96.92%	Conservative:	6
Best Local Similarity:	92.31%	Mismatches:	4
Query Match:	93.36%	Indels:	0
DB:	7	Gaps:	0

US-10-072-159-11 (1-130) x CO389083 (1-857)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||  ||||||:::||||||:::||||||||||||||||||||
Db         69 TTCAGCGTAGGGCTGGAGACCCGCGTCACTGTCCCCAATGTTCCCATTCGCTTTACTAAG 128

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATT 188

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        189 CCGGGGCTCTACTACTTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGC 248

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||:::||||||||||||||||||||||||||||    ||||||
Db        249 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAAAATGTG 308

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        309 GACCAGGCCTCTGGCTCCATGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAA 368

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||||:::  ||||||||||||||||||||  ||||||||||||||||
Db        369 GTGTATGGGGAAGGGGACAACAATGGACTCTATGCAGATAATGTCAATGACTCTACATTT 428

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        429 ACAGGCTTCCTTCTCTACCATGATACCAAC 458
```

RESULT 5
BX519230

```
LOCUS       BX519230               523 bp    mRNA    linear   EST 27-JUN-2003
DEFINITION  BX519230 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGp998D213139 ; IMAGE:1247588, mRNA sequence.
ACCESSION   BX519230
VERSION     BX519230.1  GI:32300580
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
            and Korn,B.
  TITLE     Mouse UnigeneSet - RZPD2
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998D213139.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            T7, Primer sequence: TAATACGACTCACTATAGGG.
FEATURES            Location/Qualifiers
     source         1. .523
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGp998D213139 ; IMAGE:1247588"
                    /sex="female (lactating)"
                    /tissue_type="mammary gland"
                    /lab_host="DH10B"
                    /clone_lib="Soares_mammary_gland_NMLMG"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; 1st strand cDNA was prepared from mammary
                    gland tissue from a lactating female, and was then primed
                    with a Not I - oligo(dT) primer. Double-stranded cDNA was
                    ligated to Eco RI adaptors (Pharmacia), digested with Not
                    I and cloned into the Not I and Eco RI sites of the
                    modified pT7T3 vector. Library is normalized. Library
                    was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
```

Alignment Scores:

Pred. No.:	7.75e-74	Length:	523
Score:	655.00	Matches:	119
Percent Similarity:	96.92%	Conservative:	7
Best Local Similarity:	91.54%	Mismatches:	4
Query Match:	92.51%	Indels:	0
DB:	5	Gaps:	0

US-10-072-159-11 (1-130) x BX519230 (1-523)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||  ||||||:::||||||:::||||||||||||||||||||
Db         88 TTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTTTACTAAG 147

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        148 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 207

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        208 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 267

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||:::||||||||||||||||||||||||||||    ||||||
Db        268 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTG 327

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 GACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAG 387

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||:::|||:::  ||||||||||||||||||||  ||||||||||||||||
Db        388 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 447

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        448 ACTGGCTTTCTTCTCTACCATGATACCAAC 477
```

RESULT 6
BE625509

```
LOCUS       BE625509               552 bp    mRNA    linear   EST 24-AUG-2000
DEFINITION  uu19e06.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:3372418 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
            complement-related protein Acrp30 (MOUSE);, mRNA sequence.
ACCESSION   BE625509
VERSION     BE625509.1  GI:9905925
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1082022
            Seq primer: -40RP from Gibco
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3372418"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:              8.29e-74        Length:         552
Score:                  655.00          Matches:        119
Percent Similarity:     96.92%          Conservative:   7
Best Local Similarity:  91.54%          Mismatches:     4
Query Match:            92.51%          Indels:         0
DB:                     2               Gaps:           0

US-10-072-159-11 (1-130) x BE625509 (1-552)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||  ||||||:::|||||||::|||||||||||||||||||||
Db         97 TTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTTTACTAAG 156

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        157 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 216

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        217 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 276

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||:::|||||||||||||||||||||||||   ||||||
Db        277 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTG 336

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 GACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAG 396

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||:::|||:::  ||||||||||||||||||||  ||||||||||||||||||
Db        397 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 456

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        457 ACTGGCTTTCTTCTCTACCATGATACCAAC 486

RESULT 7
AA028544
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```
LOCUS       AA028544               566 bp    mRNA    linear   EST 11-SEP-1996
DEFINITION  mi18b08.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:463863 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
            complement-related protein Acrp30 (MOUSE);, mRNA sequence.
ACCESSION   AA028544
VERSION     AA028544.1  GI:1494605
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:277679
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 492.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:463863"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
ORIGIN

Alignment Scores:
Pred. No.:              8.56e-74        Length:         566
Score:                  655.00          Matches:        119
Percent Similarity:     96.92%          Conservative:   7
Best Local Similarity:  91.54%          Mismatches:     4
Query Match:            92.51%          Indels:         0
DB:                     1               Gaps:           0

US-10-072-159-11 (1-130) x AA028544 (1-566)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||  ||||||:::|||||||::|||||||||||||||||||||
Db         28 TTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTTTACTAAG 87

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db         88 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 147

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
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Db        148 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 207

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal  80
              ||||||||||||||||||||:::||||||||||||||||||||||||||   ||||||
Db        208 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTG 267

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAG 327

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              |||||||||:::||:::  ||||||||||||||||||||  ||||||||||||||||
Db        328 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 387

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        388 ACTGGCTTTCTTCTCTACCATGATACCAAC 417
```

RESULT 8
AK003138

```
LOCUS       AK003138                921 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male heart cDNA, RIKEN full-length enriched
            library, clone:1010001N20 product:adipocyte complement related
            protein of 30 kDa, full insert sequence.
ACCESSION   AK003138
VERSION     AK003138.1  GI:12833616
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 921)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0. Second strand cDNA
            was prepared with the primer adapter of sequence[5'
            GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was
            cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
            XhoI. Host: SOLR.
FEATURES              Location/Qualifiers
     source           1. .921
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="FANTOM_DB:1010001N20"
                      /db_xref="taxon:10090"
                      /clone="1010001N20"
                      /sex="male"
                      /tissue_type="heart"
                      /clone_lib="RIKEN full-length enriched mouse cDNA library"
                      /dev_stage="adult"
     CDS              33. .776
                      /note="unnamed protein product; adipocyte complement
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                      evidence: BLASTN, 99%, match=744)
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                      /protein_id="BAB22597.1"
                      /db_xref="GI:12833617"
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                      RKGEPGEAAYVYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGL
                      YYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQV
                      YGDGDHNGLYADNVNDSTFTGFLLYHDTN"
ORIGIN
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Alignment Scores:

Pred. No.:	1.59e-73	Length:	921
Score:	655.00	Matches:	119
Percent Similarity:	96.92%	Conservative:	7
Best Local Similarity:	91.54%	Mismatches:	4
Query Match:	92.51%	Indels:	0
DB:	3	Gaps:	0

US-10-072-159-11 (1-130) x AK003138 (1-921)

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Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys  20
              ||||||||||||||||||||  ||||||:::||||||:::|||||||||||||||||||
Db        384 TTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTTTACTAAG 443
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```
Qy          21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db         444 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 503

Qy          41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
               ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         504 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 563

Qy          61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Qy          81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Qy         101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db         684 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 743

Qy         121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
               ||||||||||||||||||||||||||||||
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RESULT 9
AK041214

LOCUS	AK041214 1158 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530090P11 product:adipocyte complement related protein of 30 kDa, full insert sequence.
ACCESSION	AK041214
VERSION	AK041214.1 GI:26334296
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1158)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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                     /mol_type="mRNA"
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                     /db_xref="taxon:10090"
                     /clone="A530090P11"
                     /sex="male"
                     /tissue_type="aorta and vein"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             65. .808
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ORIGIN
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Alignment Scores:

Pred. No.:	2.12e-73	Length:	1158
Score:	655.00	Matches:	119
Percent Similarity:	96.92%	Conservative:	7
Best Local Similarity:	91.54%	Mismatches:	4
Query Match:	92.51%	Indels:	0
DB:	3	Gaps:	0

US-10-072-159-11 (1-130) x AK041214 (1-1158)

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Qy           1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
               |||||||||||||||||||||   ||||||:::||||||:::||||||||||||||||||
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Qy          21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        536 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 595

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Db        656 GACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAG 715

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        716 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 775

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
                |||||||||||||||||||||||||||||
Db        776 ACTGGCTTTCTTCTCTACCATGATACCAAC 805

RESULT 10
BM384395/c
LOCUS       BM384395                 605 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  UI-R-CN1-cjn-e-02-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone
            UI-R-CN1-cjn-e-02-0-UI 3', mRNA sequence.
ACCESSION   BM384395
VERSION     BM384395.1  GI:18184448
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized brown adipose library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com) The following repetitive
            elements were found in this cDNA sequence: 1-25,
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            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-CN1-cjn-e-02-0-UI"
                     /dev_stage="adult"
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                     /clone_lib="UI-R-CN1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
```

polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1 library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat seminal vesicles, normalized rat penis, normalized rat bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CN1 library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plamid DNA template preparation) comprising: a) a pool of about 34,000 clones from the Rat Unigene Set corresponding to plates R-5-AA-NN excluding plates R-5-MM and MN. This pool represented 40% of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CA0 and CA1 corresponding to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS, R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA, R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR, R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF, R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s and normalized libaries CS0, CT0, CU0, CW0, and CX0 corresponding to plates R-CS0s-CBD through R-CS0s-CBO, R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN, R-CU0-BUQ through R-CU0-BVL, R-CW0-BVV through R-CW0-BWP, R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM. The resulting pool represented 5% of the final driver population. d) a pool of about 5,000 clones (1,000 from non-normalized eye library CV0 and 4,000 from normalized eye library CV1) corresponding to plates R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BV0p (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDB through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH. The resulting pool represented 5% of the final driver population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI,

bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-g-08-0-UI,
bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI,
bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-c-09-0-UI,
bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI,
bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI,
blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI,
blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI,
blq-h-04-0-UI, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG_TISSUE=brown adipose
TAG_LIB=UI-R-CN1
TAG_SEQ=TTGTC"

ORIGIN

Alignment Scores:

Pred. No.:	2.27e-73	Length:	605
Score:	652.00	Matches:	119
Percent Similarity:	96.15%	Conservative:	6
Best Local Similarity:	91.54%	Mismatches:	5
Query Match:	92.09%	Indels:	0
DB:	4	Gaps:	0

US-10-072-159-11 (1-130) x BM384395 (1-605)

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Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        569 TTCAGCGTAGGGCTGGAGACCCGCGTCACTGTCNCCAATGTTCCCATTCGCTTTACTAAG 510

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATT 450

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        449 CCGGGGCTCTACTACTTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGC 390

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||:::|||||||||||||||||||||||||||    ||||||
Db        389 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAAAATGTG 330

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        329 GACCAGGCCTCTGGCTCCATGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAA 270

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||||||||:::  ||||||||||||||||||  ||||||||||||||||||||
Db        269 GTGTATGGGGAAGGGGACAACAATGGACTCTATGCAGATAATGTCAATGACTCTACATTT 210

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        209 ACAGGCTTCCTTCTCTACCATGATACCAAC 180
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RESULT 11
AI158610
LOCUS AI158610 545 bp mRNA linear EST 30-SEP-1998
DEFINITION ud29f07.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1447333 5' similar to gb:U37222 Mus musculus 30kDa adipocyte complement-related protein Acrp30 (MOUSE);, mRNA sequence.
ACCESSION AI158610
VERSION AI158610.1 GI:3687079
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 545)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:920649
Trace considered overall poor quality
Putative full length read
vector to vector length is
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .545
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1447333"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	8.74e-73	Length:	545
Score:	647.00	Matches:	117
Percent Similarity:	96.15%	Conservative:	8
Best Local Similarity:	90.00%	Mismatches:	5
Query Match:	91.38%	Indels:	0
DB:	1	Gaps:	0

US-10-072-159-11 (1-130) x AI158610 (1-545)

```
Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||:::||||||  ||||||:::|||   :::||||||||||||||||||
Db          7 TTCAGTGTGGGGGTGGAGACCCGCGTCACTGTTCCCAAGTTACCCATTCGCTTTACTAAG 66

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db         67 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 126

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        127 CCGGGACTCTACTACTTCTCTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 186

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||||:::|||||||||||||||||||||||||||    ||||||
Db        187 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTG 246

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db        247 GACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAG 306

Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
              ||||||||:::|||:::  ||||||||||||||||||||  ||||||||||||||||
Db        307 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 366

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        367 ACTGGCTTTCTTCTCTACCATGATACCAAC 396

RESULT 12
BC078720
LOCUS       BC078720                1465 bp    mRNA    linear   HTC 03-AUG-2004
DEFINITION  Rattus norvegicus cDNA clone IMAGE:7109244, containing frame-shift
            errors.
ACCESSION   BC078720
VERSION     BC078720.1  GI:50927299
KEYWORDS    HTC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1465)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1465)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution:  MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 181 Row: l Column: 7
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21426808
            This clone has the following problem: frame shifted.
FEATURES              Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              4.41e-71        Length:         1465
Score:                  638.00          Matches:        120
Percent Similarity:     96.92%          Conservative:   6
Best Local Similarity:  92.31%          Mismatches:     4
Query Match:            90.11%          Indels:         1
DB:                     3               Gaps:           0

US-10-072-159-11 (1-130) x BC078720 (1-1465).

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        383 TTCAGCGTAGGGCTGGAGACCCGCGTCACTGTCCCCAATGTTCCCATTCGCTTTACTAAG 442

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATT 502

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        503 CCGGGGCTCTACTACTTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGC 562

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
              ||||||||||||||||||:::||||||||||||||||||||||||||  ||||||
Db        563 CTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA-AATGTG 621

Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Db        682 GTGTATGGGGAAGGGGACAACAATGGACTCTATGCAGATAATGTCAATGACTCTACATTT 741

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
              ||||||||||||||||||||||||||||||
Db        742 ACAGGCTTCCTTCTCTACCATGATACCAAC 771

RESULT 13
AI105446/c
LOCUS       AI105446                543 bp    mRNA    linear   EST 20-JAN-1999
DEFINITION  EST214735 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
            RKIBK49 3' end, mRNA sequence.
ACCESSION   AI105446
VERSION     AI105446.1  GI:3709525
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 543)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: TC52707
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
```

Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES Location/Qualifiers
source 1. .543
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2030555"
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/clone="RKIBK49"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN

Alignment Scores:

Pred. No.:	1.69e-71	Length:	543
Score:	637.00	Matches:	115
Percent Similarity:	96.80%	Conservative:	6
Best Local Similarity:	92.00%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-072-159-11 (1-130) x AI105446 (1-543)

```
Qy          6 GluThrTyrValThrIleProAsnMetProIleArgPheThrLysIlePheTyrAsnGln 25
              ||||||  ||||||:::||||||:::||||||||||||||||||||||||||||||||||
Db        529 GAGACCCGCGTCACTGTCCCCAATGTTCCCATTCGCTTTACTAAGATCTTCTACAACCAA 470

Qy         26 GlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIleProGlyLeuTyrTyr 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 CAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATTCCGGGGCTCTACTAC 410

Qy         46 PheAlaTyrHisIleThrValTyrMetLysAspValLysValSerLeuPheLysLysAsp 65
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGCCTCTTCAAGAAGGAC 350

Qy         66 LysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnValAspGlnAlaSerGly 85
              ||||||:::||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        349 AAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAAAATGTGGACCAGGCCTCTGGC 290

Qy         86 SerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGlnValTyrGlyGluGly 105
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 TCCATGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAAGTGTATGGGGAAGGG 230

Qy        106 GluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPheThrGlyPheLeuLeu 125
              :::  ||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        229 GACAACAATGGACTCTATGCAGATAATGTCAATGACTCTACATTTACAGGCTTCCTTCTC 170

Qy        126 TyrHisAspThrAsn 130
              ||||||||||||||
Db        169 TACCATGATACCAAC 155
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RESULT 14
BQ189822/c
LOCUS BQ189822 577 bp mRNA linear EST 30-APR-2002
DEFINITION UI-R-CN1-cjn-e-02-0-UI.s3 UI-R-CN1 Rattus norvegicus cDNA clone UI-R-CN1-cjn-e-02-0-UI 3', mRNA sequence.
ACCESSION BQ189822
VERSION BQ189822.1 GI:20365373
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 577)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brown adipose library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .577
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CN1-cjn-e-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CN1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: Eco RI; The UI-R-CN1 library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat seminal vesicles, normalized rat penis, normalized rat bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CN1 library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plamid DNA template preparation) comprising: a) a pool of about 34,000 clones from the Rat Unigene Set corresponding to plates R-5-AA-NN excluding plates R-5-MM and MN. This pool represented 40% of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CA0 and CA1 corresponding to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS, R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA, R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR, R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF, R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s and normalized libaries CS0, CT0, CU0, CW0, and CX0 corresponding to plates R-CS0s-CBD through R-CS0s-CBO, R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN, R-CU0-BUQ through R-CU0-BVL, R-CW0-BVV through R-CW0-BWP, R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM. The resulting pool represented 5% of the final driver population. d) a pool of about 5,000 clones (1,000 from non-normalized eye library CV0 and 4,000 from normalized eye library CV1) corresponding to plates R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC,

R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BV0p (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDB through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH. The resulting pool represented 5% of the final driver population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG_TISSUE=brown adipose
TAG_LIB=UI-R-CN1
TAG_SEQ=TTGTC"

ORIGIN

Alignment Scores:

Pred. No.:	2.45e-71	Length:	577
Score:	636.00	Matches:	116
Percent Similarity:	94.62%	Conservative:	7
Best Local Similarity:	89.23%	Mismatches:	7
Query Match:	89.83%	Indels:	0
DB:	5	Gaps:	0

US-10-072-159-11 (1-130) x BQ189822 (1-577)

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Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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Db        570 TTCAGCCTAGGGCTGGAGACCCGCGTCACTGTCCCCAATGTTCCCATTCGCTTTACTACG 511

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db        510 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAATTCCACTGCAACATT 451

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
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Db        450 CCGGGGCTCTAATACTTTTCCTACCACATCACGGTGTACATGAAGGATGTGAAAGTGAGC 391

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Qy        101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
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Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Db        210 ACAGGCTTCCTTCTCTACCATGATACCAAC 181
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RESULT 15
AA763396
LOCUS AA763396 811 bp mRNA linear EST 27-JAN-1998
DEFINITION vw53g11.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1247588 5' similar to gb:U37222 Mus musculus 30kDa adipocyte complement-related protein Acrp30 (MOUSE);, mRNA sequence.
ACCESSION AA763396
VERSION AA763396.1 GI:2813143
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 811)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:661276
Putative full length read
vector to vector length is 849
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 470.

FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1247588"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	6.82e-71	Length:	811
Score:	634.00	Matches:	119
Percent Similarity:	96.92%	Conservative:	7
Best Local Similarity:	91.54%	Mismatches:	4
Query Match:	89.55%	Indels:	1

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DB:                 1           Gaps:          0

US-10-072-159-11 (1-130) x AA763396 (1-811)

Qy          1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
              ||||||||||||||||||||    ||||||:::||||||:::||||||||||||||||||
Db         57 TTCAGTGTGGGGCTGGAGACCGC-GTCACTGTTCCCAATGTACCCATTCGCTTTACTAAG 115

Qy         21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        116 ATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATT 175

Qy         41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        176 CCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGC 235

Qy         61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
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Qy         81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
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Db        356 GTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTT 415

Qy        121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
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Job time : 2981 secs
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